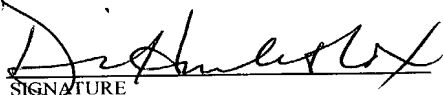


04189616 US002
526 Rec'd PCT/PTO 16 JUL 2001

FORM PTO-1390 U.S. DEPARTMENT OF COMMERCE PATENT AND TRADEMARK OFFICE		ATTORNEY'S DOCKET NUMBER PF-0662 USN
TRANSMITTAL LETTER TO THE UNITED STATES DESIGNATED/ELECTED OFFICE (DO/EO/US) CONCERNING A FILING UNDER 35 U.S.C. 371		U.S. APPLICATION NO. (If known, see 37 CFR 1.5) TO BE ASSIGNED 09/889616
INTERNATIONAL APPLICATION NO PCT/US00/02237	INTERNATIONAL FILING DATE 28 January 2000	PRIORITY DATE CLAIMED 29 January 1999
TITLE OF INVENTION CANCER-ASSOCIATED PROTEINS		
APPLICANT(S) FOR DO/EO/US INCYTE PHARMACEUTICALS, INC.; TANG, Y. Tom; LAL, Preeti; HILLMAN, Jennifer L.; YUE, Henry; AZIMZAI, Valda; LU, Dyung Aina M.; BAUGHN, Mariah R.; TRAN, Bao; SHIH, Leo L.; AU-YOUNG, Janice		
<p>Applicant herewith submits to the United States Designated/Elected Office (DO/EO/US) the following items and other information:</p> <ol style="list-style-type: none"> <input checked="" type="checkbox"/> This is the FIRST submission of items concerning a filing under 35 U.S.C. 371. <input type="checkbox"/> This is a SECOND or SUBSEQUENT submission of items concerning a filing under 35 U.S.C. 371. <input type="checkbox"/> This is an express request to promptly begin national examination procedures (35 U.S.C. 371 (f)). <input type="checkbox"/> The US has been elected by the expiration of 19 months from the priority date (PCT Article 31). <input checked="" type="checkbox"/> A copy of the International Application as filed (35 U.S.C. 371(c)(2)) <ol style="list-style-type: none"> <input type="checkbox"/> is attached hereto (required only if not communicated by the International Bureau) <input type="checkbox"/> has been communicated by the International Bureau. <input checked="" type="checkbox"/> is not required, as the application was filed in the United States Receiving Office (RO/US). <input type="checkbox"/> An English language translation of the International Application as filed (35 U.S.C. 371(c)(2)). <input checked="" type="checkbox"/> Amendments to the claims of the International Application under PCT Article 19 (35 U.S.C. 371(c)(3)) <ol style="list-style-type: none"> <input type="checkbox"/> are attached hereto (required only if not communicated by the International Bureau). <input type="checkbox"/> have been communicated by the International Bureau. <input type="checkbox"/> have not been made; however, the time limit for making such amendments has NOT expired. <input checked="" type="checkbox"/> have not been made and will not be made. <input type="checkbox"/> An English language translation of the amendments to the claims under PCT Article 19 (35 U.S.C. 371(c)(3)). <input type="checkbox"/> An oath or declaration of the inventor(s) (35 U.S.C. 371(c)(4)). <input type="checkbox"/> An English language translation of the annexes to the International Preliminary Examination Report under PCT Article 36 (35 U.S.C. 371(c)(5)). 		
Items 11 to 16 below concern document(s) or information included:		
<ol style="list-style-type: none"> <input type="checkbox"/> An Information Disclosure Statement under 37 CFR 1.97 and 1.98. <input type="checkbox"/> An assignment document for recording. A separate cover sheet in compliance with 37 CFR 3.27 and 3.31 is included. <input type="checkbox"/> A FIRST preliminary amendment. <ul style="list-style-type: none"> <input type="checkbox"/> A SECOND or SUBSEQUENT preliminary amendment. <input type="checkbox"/> A substitute specification. <input type="checkbox"/> A change of power of attorney and/or address letter. <input checked="" type="checkbox"/> Other items or information: <ol style="list-style-type: none"> Transmittal Letter (2 pp, in duplicate) Return Postcard Express Mail Label No.: EL 856 154 129 US Request to Transfer 		

4438936 1.6 1050137
JC18 Rec'd PCT/PTO 1 6 JUL 2001

U.S. APPLICATION NO. (if known) (37 CFR 1.53) 09/ 889616 TO BE ASSIGNED		INTERNATIONAL APPLICATION NO. PCT/US00/02237		ATTORNEY'S DOCKET NUMBER PF-0662 USN	
17. <input checked="" type="checkbox"/> The following fees are submitted BASIC NATIONAL FEE (37 CFR 1.492(a)(1)-(5)): Neither international preliminary examination fee (37 CFR 1.482) nor international search fee (37 CFR 1.445(a)(2)) paid to USPTO and International Search Report not prepared by the EPO or JPO . . . \$1000.00 <input type="checkbox"/> International preliminary examination fee (37 CFR 1.482) not paid to USPTO but International Search Report prepared by the EPO or JPO. \$860.00 International preliminary examination fee (37 CFR 1.482) not paid to USPTO but international search fee (37 CFR 1.445(a)(2)) paid to USPTO. . . \$710.00 <input checked="" type="checkbox"/> International preliminary examination fee paid to USPTO (37 CFR 1.482) but all claims did not satisfy provisions of PCT Article 33(1)-(4). . . \$690.00 <input type="checkbox"/> International preliminary examination fee paid to USPTO (37 CFR 1.482) and all claims satisfied provisions of PCT Article 33(1)-(4). . . \$100.00					
ENTER APPROPRIATE BASIC FEE AMOUNT =				\$690.00	
Surcharge of \$130.00 for furnishing the oath or declaration later than <input type="checkbox"/> 20 <input type="checkbox"/> 30 months from the earliest claimed priority date (37 CFR 1.492(e)).				\$	
CLAIMS	NUMBER FILED	NUMBER EXTRA	RATE		
Total Claims	23 =	3	X \$ 18.00	\$ 54.00	
Independent Claims	2 =	0	X \$ 80.00	\$	
MULTIPLE DEPENDENT CLAIM(S) (if applicable)			+ \$270.00	\$	
TOTAL OF ABOVE CALCULATIONS =				\$744.00	
<input type="checkbox"/> Applicant claims small entity status. See 37 CFR 1.27. The fees indicated above are reduced by 1/2.				\$	
SUBTOTAL =				\$744.00	
Processing fee of \$130.00 for furnishing the English translation later than <input type="checkbox"/> 20 <input type="checkbox"/> 30 months from the earliest claimed priority date (37 CFR 1.492(f)).				\$	
TOTAL NATIONAL FEE =				\$744.00	
Fee for recording the enclosed assignment (37 CFR 1.21(h)). The assignment must be accompanied by the appropriate cover sheet (37 CFR 3.28, 3.31) \$40.00 per property +				\$	
TOTAL FEES ENCLOSED =				\$744.00	
				Amount to be Refunded	\$
				Charged	\$
a. <input type="checkbox"/> A check in the amount of \$ _____ to cover the above fees is enclosed. b. <input checked="" type="checkbox"/> Please charge my Deposit Account No. <u>09-0108</u> in the amount of \$ <u>744.00</u> to cover the above fees c. <input checked="" type="checkbox"/> The Commissioner is hereby authorized to charge any additional fees which may be required, or credit any overpayment to Deposit Account No. <u>09-0108</u> . A duplicate copy of this sheet is enclosed. NOTE: Where an appropriate time limit under 37 CFR 1.494 or 1.495 has not been met, a petition to revive (37 CFR 1.137(a) or (b)) must be filed and granted to restore the application to pending status. SEND ALL CORRESPONDENCE TO INCYTE GENOMICS, INC. 3160 Porter Drive Palo Alto, CA 94304 <div style="text-align: center; margin-top: 20px;">  SIGNATURE NAME: Diana Hamlet-Cox REGISTRATION NUMBER: 33,302 DATE: <u>16</u> July 2001 </div>					

NUCLEIC-ACID BINDING PROTEINS

TECHNICAL FIELD

This invention relates to nucleic acid and amino acid sequences of nucleic-acid binding proteins and to the use of these sequences in the diagnosis, treatment, and prevention of reproductive, immune, and neurological disorders, and cell proliferative disorders including cancer.

5

BACKGROUND OF THE INVENTION

Multicellular organisms are comprised of diverse cell types that differ dramatically both in structure and function. The identity of a cell is determined by its characteristic pattern of gene expression, and different cell types express overlapping but distinct sets of genes throughout development. Spatial and temporal regulation of gene expression is critical for the control of cell proliferation, cell differentiation, apoptosis, and other processes that contribute to organismal development. Furthermore, gene expression is regulated in response to extracellular signals that mediate cell-cell communication and coordinate the activities of different cell types. Appropriate gene regulation also ensures that cells function efficiently by expressing only those genes whose functions are required at a given time.

Transcriptional regulatory proteins are essential for the control of gene expression. Some of these proteins function as transcription factors that initiate, activate, repress, or terminate gene transcription. Transcription factors generally bind to promoter, enhancer, or upstream regulatory regions of a gene in a sequence-specific manner, although some factors bind regulatory elements within or downstream of the coding region. Transcription factors may bind to a specific region of DNA singly or as a complex with other accessory factors. (Reviewed in Lewin, B. (1990) Genes IV, Oxford University Press, New York, NY, pp. 554-570.)

The double helix structure and repeated sequences of DNA create topological and chemical features which can be recognized by transcription factors. These features include hydrogen bond donor and acceptor groups, hydrophobic patches, major and minor grooves, and regular repeated stretches of sequence which induce distinct bends in the helix. Typically, transcription factors recognize specific DNA sequence motifs of about 20 nucleotides in length. Multiple adjacent transcription factor-binding motifs may be required for gene regulation.

Many transcription factors incorporate DNA-binding structural motifs which comprise either α helices or β sheets that bind to the major groove of DNA. Four well-characterized structural motifs are helix-turn-helix, zinc finger, leucine zipper, and helix-loop-helix. Proteins containing these motifs may act alone as monomers or form homo- or heterodimers that interact with DNA.

The helix-turn-helix motif consists of two α helices connected at a fixed angle by a short

chain of amino acids. One of the helices binds to the major groove. Helix-turn-helix motifs are exemplified by the homeobox motif which is present in homeodomain proteins. These proteins are critical for specifying the anterior-posterior body axis during development and are conserved throughout the animal kingdom. The Antennapedia and Ultrabithorax proteins of Drosophila melanogaster are prototypical homeodomain proteins. (Pabo, C.O. and R.T. Sauer (1992) Ann. Rev. Biochem. 61:1053-1095.)

The zinc finger motif, which binds zinc ions, generally contains tandem repeats of about 30 amino acids consisting of periodically spaced cysteine and histidine residues. Examples of this sequence pattern include the C2H2-type and the C3HC4-type zinc fingers, and the PHD domain.

(Lewin, supra ; Aasland, R., et al. (1995) Trends Biochem. Sci 20:56 - 59.) Zinc finger proteins each contain an α helix and an antiparallel β sheet whose proximity and conformation are maintained by the zinc ion. Contact with DNA is made by the arginine preceding the α helix and by the second, third, and sixth residues of the α helix. Variants of the zinc finger motif include poorly defined cysteine-rich motifs which bind zinc or other metal ions. These motifs may not contain histidine residues and are generally nonrepetitive.

The leucine zipper motif comprises a stretch of amino acids rich in leucine which can form an amphipathic α helix. This structure provides the basis for dimerization of two leucine zipper proteins. The region adjacent to the leucine zipper is usually basic, and upon protein dimerization, is optimally positioned for binding to the major groove. Proteins containing such motifs are generally referred to as bZIP transcription factors.

The helix-loop-helix motif (HLH) consists of a short α helix connected by a loop to a longer α helix. The loop is flexible and allows the two helices to fold back against each other and to bind to DNA. The transcription factor Myc contains a prototypical HLH motif.

Most transcription factors contain characteristic DNA binding motifs, and variations on the above motifs and new motifs have been and are currently being characterized. (Faisst, S. and S. Meyer (1992) Nucl. Acids Res. 20:3-26.)

Mutations in transcription factors contribute to oncogenesis. This is likely due to the role of transcription factors in the expression of genes involved in cell proliferation. For example, mutations in transcription factors encoded by proto-oncogenes, such as Fos, Jun, Myc, Rel, and Sp1, may be oncogenic due to increased stimulation of cell proliferation. Conversely, mutations in transcription factors encoded by tumor suppressor genes, such as p53, RB1, and WT1, may be oncogenic due to decreased inhibition of cell proliferation. (Latchman, D. (1995) Gene Regulation: A Eukaryotic Perspective, Chapman and Hall, London, UK, pp 242-255.)

Gene expression is also affected by chromatin-associated proteins. In the nucleus, DNA is

packaged into chromatin, the compact organization of which limits the accessibility of DNA to transcription factors and plays a key role in gene regulation. (Lewin, supra, pp. 409-410.) The compact structure of chromatin is determined and influenced by chromatin-associated proteins such as histones, high mobility group (HMG) proteins, helicases, and chromodomain proteins. There are five classes of histones, H1, H2A, H2B, H3, and H4, all of which are highly basic, low molecular weight proteins. The fundamental unit of chromatin, the nucleosome, consists of 200 base pairs of DNA associated with two copies each of H2A, H2B, H3, and H4. H1 links adjacent nucleosomes. HMG proteins are low molecular weight, non-histone proteins that may play a role in unwinding DNA and stabilizing single-stranded DNA. Helicases, which are DNA-dependent ATPases, unwind DNA, allowing access for transcription factors. Chromodomain proteins play a key role in the formation of highly-compacted, transcriptionally silent heterochromatin.

Much of the regulation of gene expression in eucaryotic cells occurs at the posttranscriptional level. Messenger RNAs (mRNA), which are produced in the cell nucleus from primary transcripts of protein-encoding genes, are processed and transported to the cytoplasm where the protein synthesis machinery is located. RNA-binding proteins are a group of proteins that participate in the processing, editing, transport, localization, and posttranscriptional regulation of mRNAs, and comprise the protein component of ribosomes as well. The RNA-binding activity of many of these proteins is mediated by a series of RNA-binding motifs identified within them. These domains include the RNP motif, the arginine-rich motif, the RGG box, and the KH motif. (Reviewed in Burd, C. G. and Dreyfuss, G. (1994) Science 265:615 - 621.) The RNP motif is the most widely found and best characterized of these motifs. The RNP motif is composed of 90-100 amino acids which form an RNA-binding domain and is found in one or more copies in proteins that bind pre-mRNA, mRNA, pre-ribosomal RNA, and small nuclear RNAs. The RNP motif is composed of two short sequences (RNP-1 and RNP-2) and a number of other mostly hydrophobic, conserved amino acids interspersed throughout the motif. (Burd, supra; ExPASy PROSITE document PDOC0030.)

Many neoplastic disorders in humans can be attributed to inappropriate gene expression. Malignant cell growth may result from either excessive expression of tumor promoting genes or insufficient expression of tumor suppressor genes. (Cleary, M.L. (1992) Cancer Surv. 15:89-104.) Chromosomal translocations may also produce chimeric loci which fuse the coding sequence of one gene with the regulatory regions of a second unrelated gene. Such an arrangement often results in inappropriate gene transcription. The Wilms tumor suppressor gene product, WT1, is a protein containing a DNA-binding domain consisting of four zinc fingers and a proline-glutamine rich region capable of regulating transcription. (ExPASy PROSITE document PR00049.) Deletions of the WT1 gene, or point mutations which destroy the DNA-binding activity of the protein are associated with development of the pediatric nephroblastoma, Wilms tumor, and Denys-Drash syndrome. (Rauscher,

F.J. (1993) FASEB J. 7:896-903.)

Certain proteins enriched in glutamine are associated with various neurological disorders including spinocerebellar ataxia, bipolar effective disorder, schizophrenia, and autism. (Margolis, R.L. et al. (1997) Human Genetics 100:114-122.) These proteins contain regions with as many as 15 or more consecutive glutamine residues and may function as transcription factors with a potential role in regulation of neurodevelopment or neuroplasticity.

The immune system responds to infection or trauma by activating a cascade of events that coordinate the progressive selection, amplification, and mobilization of cellular defense mechanisms. A complex and balanced program of gene activation and repression is involved in this process. However, hyperactivity of the immune system as a result of improper or insufficient regulation of gene expression may result in considerable tissue or organ damage. This damage is well documented in immunological responses associated with arthritis, allergens, heart attack, stroke, and infections. (Harrison's Principles of Internal Medicine, 13/e, McGraw Hill, Inc. and Teton Data Systems Software, 1996.) In particular, a zinc finger protein termed Staf50 (for Stimulated trans-acting factor of 50 kDa) is a transcriptional regulator and is induced in various cell lines by interferon-I and -II. Staf50 appears to mediate the antiviral activity of interferon by down-regulating the viral transcription directed by the long terminal repeat promoter region of human immunodeficiency virus type-1 in transfected cells. (Tissot, C. (1995) J. Biol. Chem. 270:14891-14898.)

Furthermore, the generation of multicellular organisms is based upon the induction and coordination of cell differentiation at the appropriate stages of development. Central to this process is differential gene expression, which confers the distinct identities of cells and tissues throughout the body. Failure to regulate gene expression during development could result in developmental disorders.

The discovery of new nucleic-acid binding proteins and the polynucleotides encoding them satisfies a need in the art by providing new compositions which are useful in the diagnosis, prevention, and treatment of reproductive, immune, and neurological disorders, and cell proliferative disorders including cancer.

SUMMARY OF THE INVENTION

The invention features purified polypeptides, protnames, referred to collectively as "ABBR" and individually as "NuABP-1," "NuABP-2," "NuABP-3," "NuABP-4," "NuABP-5," "NuABP-6," "NuABP-7," "NuABP-8," "NuABP-9," "NuABP-10," "NuABP-11," "NuABP-12," "NuABP-13," "NuABP-14," "NuABP-15," "NuABP-16," "NuABP-17," "NuABP-18," "NuABP-19," "NuABP-20," "NuABP-21," "NuABP-22," "NuABP-23," "NuABP-24," "NuABP-25," "NuABP-26," "NuABP-27," "NuABP-28," "NuABP-29," "NuABP-30," "NuABP-31," "NuABP-32," "NuABP-33,"

“NuABP-34,” “NuABP-35,” “NuABP-36,” “NuABP-37,” “NuABP-38,” “NuABP-39,” “NuABP-40,” “NuABP-41,” “NuABP-42,” “NuABP-43,” “NuABP-44,” “NuABP-45,” “NuABP-46,” “NuABP-47,” “NuABP-48,” “NuABP-49,” “NuABP-50,” “NuABP-51,” “NuABP-52,” “NuABP-53,” “NuABP-54,” and “NuABP-55.” In one aspect, the invention provides an isolated polypeptide comprising a) an amino acid sequence selected from the group consisting of SEQ ID NO:1-55, b) a naturally occurring amino acid sequence having at least 90% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NO:1-55, c) a biologically active fragment of an amino acid sequence selected from the group consisting of SEQ ID NO:1-55, or d) an immunogenic fragment of an amino acid sequence selected from the group consisting of SEQ ID NO:1-55. In one alternative, the invention provides an isolated polypeptide comprising the amino acid sequence of SEQ ID NO:1-55.

The invention further provides an isolated polynucleotide encoding a polypeptide comprising a) an amino acid sequence selected from the group consisting of SEQ ID NO:1-55, b) a naturally occurring amino acid sequence having at least 90% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NO:1-55, c) a biologically active fragment of an amino acid sequence selected from the group consisting of SEQ ID NO:1-55, or d) an immunogenic fragment of an amino acid sequence selected from the group consisting of SEQ ID NO:1-55. In one alternative, the polynucleotide is selected from the group consisting of SEQ ID NO:56-110.

Additionally, the invention provides a recombinant polynucleotide comprising a promoter sequence operably linked to a polynucleotide encoding a polypeptide comprising a) an amino acid sequence selected from the group consisting of SEQ ID NO:1-55, b) a naturally occurring amino acid sequence having at least 90% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NO:1-55, c) a biologically active fragment of an amino acid sequence selected from the group consisting of SEQ ID NO:1-55, or d) an immunogenic fragment of an amino acid sequence selected from the group consisting of SEQ ID NO:1-55. In one alternative, the invention provides a cell transformed with the recombinant polynucleotide. In another alternative, the invention provides a transgenic organism comprising the recombinant polynucleotide.

The invention also provides a method for producing a polypeptide comprising a) an amino acid sequence selected from the group consisting of SEQ ID NO:1-55, b) a naturally occurring amino acid sequence having at least 90% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NO:1-55, c) a biologically active fragment of an amino acid sequence selected from the group consisting of SEQ ID NO:1-55, or d) an immunogenic fragment of an amino acid sequence selected from the group consisting of SEQ ID NO:1-55. The method comprises a) culturing a cell under conditions suitable for expression of the polypeptide, wherein said cell is transformed with a recombinant polynucleotide comprising a promoter sequence operably linked to a polynucleotide encoding the polypeptide, and b) recovering the polypeptide so expressed.

The invention also provides a method for screening a compound for effectiveness as an agonist of a polypeptide comprising a) an amino acid sequence selected from the group consisting of SEQ ID NO:1-55, b) a naturally occurring amino acid sequence having at least 90% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NO:1-55, c) a biologically active fragment of an amino acid sequence selected from the group consisting of SEQ ID NO:1-55, or d) an immunogenic fragment of an amino acid sequence selected from the group consisting of SEQ ID NO:1-55. The method comprises a) exposing a sample comprising the polypeptide to a compound, and b) detecting agonist activity in the sample. In one alternative, the invention provides a pharmaceutical composition comprising an agonist compound identified by the method and a pharmaceutically acceptable excipient. In another alternative, the invention provides a method of treating a disease or condition associated with decreased expression of functional NuABP, comprising administering to a patient in need of such treatment the pharmaceutical composition.

Additionally, the invention provides a method for screening a compound for effectiveness as an antagonist of a polypeptide comprising a) an amino acid sequence selected from the group consisting of SEQ ID NO:1-55, b) a naturally occurring amino acid sequence having at least 90% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NO:1-55, c) a biologically active fragment of an amino acid sequence selected from the group consisting of SEQ ID NO:1-55, or d) an immunogenic fragment of an amino acid sequence selected from the group consisting of SEQ ID NO:1-55. The method comprises a) exposing a sample comprising the polypeptide to a compound, and b) detecting antagonist activity in the sample. In one alternative, the invention provides a pharmaceutical composition comprising an antagonist compound identified by the method and a pharmaceutically acceptable excipient. In another alternative, the invention provides a method of treating a disease or condition associated with overexpression of functional NuABP, comprising administering to a patient in need of such treatment the pharmaceutical composition.

The invention further provides a method for screening a compound for effectiveness in altering expression of a target polynucleotide, wherein said target polynucleotide comprises a sequence selected from the group consisting of SEQ ID NO:56-110, the method comprising a) exposing a sample comprising the target polynucleotide to a compound, and b) detecting altered expression of the target polynucleotide.

BRIEF DESCRIPTION OF THE TABLES

Table 1 shows polypeptide and nucleotide sequence identification numbers (SEQ ID NOs), clone identification numbers (clone IDs), cDNA libraries, and cDNA fragments used to assemble full-length sequences encoding NuABP.

Table 2 shows features of each polypeptide sequence, including potential motifs, homologous sequences, and methods, algorithms, and searchable databases used for analysis of NuABP.

Table 3 shows selected fragments of each nucleic acid sequence: the tissue-specific expression patterns of each nucleic acid sequence as determined by northern analysis; diseases, disorders, or conditions associated with these tissues; and the vector into which each cDNA was cloned.

Table 4 describes the tissues used to construct the cDNA libraries from which cDNA clones encoding NuABP were isolated.

Table 5 shows the tools, programs, and algorithms used to analyze NuABP, along with applicable descriptions, references, and threshold parameters.

DESCRIPTION OF THE INVENTION

Before the present proteins, nucleotide sequences, and methods are described, it is understood that this invention is not limited to the particular machines, materials and methods described, as these may vary. It is also to be understood that the terminology used herein is for the purpose of describing particular embodiments only, and is not intended to limit the scope of the present invention which will be limited only by the appended claims.

It must be noted that as used herein and in the appended claims, the singular forms "a," "an," and "the" include plural reference unless the context clearly dictates otherwise. Thus, for example, a reference to "a host cell" includes a plurality of such host cells, and a reference to "an antibody" is a reference to one or more antibodies and equivalents thereof known to those skilled in the art, and so forth.

Unless defined otherwise, all technical and scientific terms used herein have the same meanings as commonly understood by one of ordinary skill in the art to which this invention belongs. Although any machines, materials, and methods similar or equivalent to those described herein can be used to practice or test the present invention, the preferred machines, materials and methods are now described. All publications mentioned herein are cited for the purpose of describing and disclosing the cell lines, protocols, reagents and vectors which are reported in the publications and which might be used in connection with the invention. Nothing herein is to be construed as an admission that the invention is not entitled to antedate such disclosure by virtue of prior invention.

DEFINITIONS

"NuABP" refers to the amino acid sequences of substantially purified NuABP obtained from any species, particularly a mammalian species, including bovine, ovine, porcine, murine, equine, and human, and from any source, whether natural, synthetic, semi-synthetic, or recombinant.

The term "agonist" refers to a molecule which intensifies or mimics the biological activity of

NuABP. Agonists may include proteins, nucleic acids, carbohydrates, small molecules, or any other compound or composition which modulates the activity of NuABP either by directly interacting with NuABP or by acting on components of the biological pathway in which NuABP participates.

An "allelic variant" is an alternative form of the gene encoding NuABP. Allelic variants may result from at least one mutation in the nucleic acid sequence and may result in altered mRNAs or in polypeptides whose structure or function may or may not be altered. A gene may have none, one, or many allelic variants of its naturally occurring form. Common mutational changes which give rise to allelic variants are generally ascribed to natural deletions, additions, or substitutions of nucleotides. Each of these types of changes may occur alone, or in combination with the others, one or more times in a given sequence.

"Altered" nucleic acid sequences encoding NuABP include those sequences with deletions, insertions, or substitutions of different nucleotides, resulting in a polypeptide the same as NuABP or a polypeptide with at least one functional characteristic of NuABP. Included within this definition are polymorphisms which may or may not be readily detectable using a particular oligonucleotide probe of the polynucleotide encoding NuABP, and improper or unexpected hybridization to allelic variants, with a locus other than the normal chromosomal locus for the polynucleotide sequence encoding NuABP. The encoded protein may also be "altered," and may contain deletions, insertions, or substitutions of amino acid residues which produce a silent change and result in a functionally equivalent NuABP. Deliberate amino acid substitutions may be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity, and/or the amphipathic nature of the residues, as long as the biological or immunological activity of NuABP is retained. For example, negatively charged amino acids may include aspartic acid and glutamic acid, and positively charged amino acids may include lysine and arginine. Amino acids with uncharged polar side chains having similar hydrophilicity values may include: asparagine and glutamine; and serine and threonine. Amino acids with uncharged side chains having similar hydrophilicity values may include: leucine, isoleucine, and valine; glycine and alanine; and phenylalanine and tyrosine.

The terms "amino acid" and "amino acid sequence" refer to an oligopeptide, peptide, polypeptide, or protein sequence, or a fragment of any of these, and to naturally occurring or synthetic molecules. Where "amino acid sequence" is recited to refer to an amino acid sequence of a naturally occurring protein molecule, "amino acid sequence" and like terms are not meant to limit the amino acid sequence to the complete native amino acid sequence associated with the recited protein molecule.

"Amplification" relates to the production of additional copies of a nucleic acid sequence. Amplification is generally carried out using polymerase chain reaction (PCR) technologies well known in the art.

The term "antagonist" refers to a molecule which inhibits or attenuates the biological activity of NuABP. Antagonists may include proteins such as antibodies, nucleic acids, carbohydrates, small molecules, or any other compound or composition which modulates the activity of NuABP either by directly interacting with NuABP or by acting on components of the biological pathway in which NuABP participates.

The term "antibody" refers to intact immunoglobulin molecules as well as to fragments thereof, such as Fab, F(ab')₂, and Fv fragments, which are capable of binding an epitopic determinant. Antibodies that bind NuABP polypeptides can be prepared using intact polypeptides or using fragments containing small peptides of interest as the immunizing antigen. The polypeptide or oligopeptide used to immunize an animal (e.g., a mouse, a rat, or a rabbit) can be derived from the translation of RNA, or synthesized chemically, and can be conjugated to a carrier protein if desired. Commonly used carriers that are chemically coupled to peptides include bovine serum albumin, thyroglobulin, and keyhole limpet hemocyanin (KLH). The coupled peptide is then used to immunize the animal.

The term "antigenic determinant" refers to that region of a molecule (i.e., an epitope) that makes contact with a particular antibody. When a protein or a fragment of a protein is used to immunize a host animal, numerous regions of the protein may induce the production of antibodies which bind specifically to antigenic determinants (particular regions or three-dimensional structures on the protein). An antigenic determinant may compete with the intact antigen (i.e., the immunogen used to elicit the immune response) for binding to an antibody.

The term "antisense" refers to any composition containing a nucleic acid sequence which is complementary to the "sense" strand of a specific nucleic acid sequence. Antisense molecules may be produced by any method including synthesis or transcription. Once introduced into a cell, the complementary nucleotides combine with natural sequences produced by the cell to form duplexes and to block either transcription or translation. The designation "negative" or "minus" can refer to the antisense strand, and the designation "positive" or "plus" can refer to the sense strand.

The term "biologically active" refers to a protein having structural, regulatory, or biochemical functions of a naturally occurring molecule. Likewise, "immunologically active" refers to the capability of the natural, recombinant, or synthetic NuABP, or of any oligopeptide thereof, to induce a specific immune response in appropriate animals or cells and to bind with specific antibodies.

The terms "complementary" and "complementarity" refer to the natural binding of polynucleotides by base pairing. For example, the sequence "5' A-G-T 3'" bonds to the complementary sequence "3' T-C-A 5'." Complementarity between two single-stranded molecules may be "partial," such that only some of the nucleic acids bind, or it may be "complete," such that total complementarity exists between the single stranded molecules. The degree of complementarity

12

fragment of SEQ ID NO:1-55 comprises a region of unique amino acid sequence that specifically identifies SEQ ID NO:1-55. For example, a fragment of SEQ ID NO:1-55 is useful as an immunogenic peptide for the development of antibodies that specifically recognize SEQ ID NO:1-55. The precise length of a fragment of SEQ ID NO:1-55 and the region of SEQ ID NO:1-55 to which the
5 fragment corresponds are routinely determinable by one of ordinary skill in the art based on the intended purpose for the fragment.

The term "similarity" refers to a degree of complementarity. There may be partial similarity or complete similarity. The word "identity" may substitute for the word "similarity." A partially complementary sequence that at least partially inhibits an identical sequence from hybridizing to a
10 target nucleic acid is referred to as "substantially similar." The inhibition of hybridization of the completely complementary sequence to the target sequence may be examined using a hybridization assay (Southern or northern blot, solution hybridization, and the like) under conditions of reduced stringency. A substantially similar sequence or hybridization probe will compete for and inhibit the binding of a completely similar (identical) sequence to the target sequence under conditions of
15 reduced stringency. This is not to say that conditions of reduced stringency are such that non-specific binding is permitted, as reduced stringency conditions require that the binding of two sequences to one another be a specific (i.e., a selective) interaction. The absence of non-specific binding may be tested by the use of a second target sequence which lacks even a partial degree of complementarity (e.g., less than about 30% similarity or identity). In the absence of non-specific binding, the
20 substantially similar sequence or probe will not hybridize to the second non-complementary target sequence.

The phrases "percent identity" and "% identity," as applied to polynucleotide sequences, refer to the percentage of residue matches between at least two polynucleotide sequences aligned using a standardized algorithm. Such an algorithm may insert, in a standardized and reproducible way, gaps
25 in the sequences being compared in order to optimize alignment between two sequences, and therefore achieve a more meaningful comparison of the two sequences.

Percent identity between polynucleotide sequences may be determined using the default parameters of the CLUSTAL V algorithm as incorporated into the MEGALIGN version 3.12e sequence alignment program. This program is part of the LASERGENE software package, a suite of
30 molecular biological analysis programs (DNASTAR, Madison WI). CLUSTAL V is described in Higgins, D.G. and P.M. Sharp (1989) CABIOS 5:151-153 and in Higgins, D.G. et al. (1992) CABIOS 8:189-191. For pairwise alignments of polynucleotide sequences, the default parameters are set as follows: Ktuple=2, gap penalty=5, window=4, and "diagonals saved"=4. The "weighted" residue weight table is selected as the default. Percent identity is reported by CLUSTAL V as the "percent
35 similarity" between aligned polynucleotide sequence pairs.

Alternatively, a suite of commonly used and freely available sequence comparison algorithms is provided by the National Center for Biotechnology Information (NCBI) Basic Local Alignment Search Tool (BLAST) (Altschul, S.F. et al. (1990) J. Mol. Biol. 215:403-410), which is available from several sources, including the NCBI, Bethesda, MD, and on the Internet at

5 <http://www.ncbi.nlm.nih.gov/BLAST/>. The BLAST software suite includes various sequence analysis programs including "blastn," that is used to align a known polynucleotide sequence with other polynucleotide sequences from a variety of databases. Also available is a tool called "BLAST 2 Sequences" that is used for direct pairwise comparison of two nucleotide sequences. "BLAST 2 Sequences" can be accessed and used interactively at <http://www.ncbi.nlm.nih.gov/gorf/bl2.html>. The
10 "BLAST 2 Sequences" tool can be used for both blastn and blastp (discussed below). BLAST programs are commonly used with gap and other parameters set to default settings. For example, to compare two nucleotide sequences, one may use blastn with the "BLAST 2 Sequences" tool Version 2.0.9 (May-07-1999) set at default parameters. Such default parameters may be, for example:

Matrix: BLOSUM62

15 *Reward for match: 1*

Penalty for mismatch: -2

Open Gap: 5 and Extension Gap: 2 penalties

Gap x drop-off: 50

Expect: 10

20 *Word Size: 11*

Filter: on

Percent identity may be measured over the length of an entire defined sequence, for example, as defined by a particular SEQ ID number, or may be measured over a shorter length, for example, over the length of a fragment taken from a larger, defined sequence, for instance, a fragment of at
25 least 20, at least 30, at least 40, at least 50, at least 70, at least 100, or at least 200 contiguous nucleotides. Such lengths are exemplary only, and it is understood that any fragment length supported by the sequences shown herein, in the tables, figures, or Sequence Listing, may be used to describe a length over which percentage identity may be measured.

Nucleic acid sequences that do not show a high degree of identity may nevertheless encode
30 similar amino acid sequences due to the degeneracy of the genetic code. It is understood that changes in a nucleic acid sequence can be made using this degeneracy to produce multiple nucleic acid sequences that all encode substantially the same protein.

The phrases "percent identity" and "% identity," as applied to polypeptide sequences, refer to the percentage of residue matches between at least two polypeptide sequences aligned using a
35 standardized algorithm. Methods of polypeptide sequence alignment are well-known. Some

alignment methods take into account conservative amino acid substitutions. Such conservative substitutions, explained in more detail above, generally preserve the hydrophobicity and acidity at the site of substitution, thus preserving the structure (and therefore function) of the polypeptide.

Percent identity between polypeptide sequences may be determined using the default parameters of the CLUSTAL V algorithm as incorporated into the MEGALIGN version 3.12e sequence alignment program (described and referenced above). For pairwise alignments of polypeptide sequences using CLUSTAL V, the default parameters are set as follows: Ktuple=1, gap penalty=3, window=5, and "diagonals saved"=5. The PAM250 matrix is selected as the default residue weight table. As with polynucleotide alignments, the percent identity is reported by CLUSTAL V as the "percent similarity" between aligned polypeptide sequence pairs.

Alternatively the NCBI BLAST software suite may be used. For example, for a pairwise comparison of two polypeptide sequences, one may use the "BLAST 2 Sequences" tool Version 2.0.9 (May-07-1999) with blastp set at default parameters. Such default parameters may be, for example:

Matrix: BLOSUM62

Open Gap: 11 and Extension Gap: 1 penalties

Gap x drop-off: 50

Expect: 10

Word Size: 3

Filter: on

Percent identity may be measured over the length of an entire defined polypeptide sequence, for example, as defined by a particular SEQ ID number, or may be measured over a shorter length, for example, over the length of a fragment taken from a larger, defined polypeptide sequence, for instance, a fragment of at least 15, at least 20, at least 30, at least 40, at least 50, at least 70 or at least 150 contiguous residues. Such lengths are exemplary only, and it is understood that any fragment length supported by the sequences shown herein, in the tables, figures or Sequence Listing, may be used to describe a length over which percentage identity may be measured.

"Human artificial chromosomes" (HACs) are linear microchromosomes which may contain DNA sequences of about 6 kb to 10 Mb in size, and which contain all of the elements required for stable mitotic chromosome segregation and maintenance.

The term "humanized antibody" refers to antibody molecules in which the amino acid sequence in the non-antigen binding regions has been altered so that the antibody more closely resembles a human antibody, and still retains its original binding ability.

"Hybridization" refers to the process by which a polynucleotide strand anneals with a complementary strand through base pairing under defined hybridization conditions. Specific

hybridization is an indication that two nucleic acid sequences share a high degree of identity. Specific

hybridization complexes form under permissive annealing conditions and remain hybridized after the "washing" step(s). The washing step(s) is particularly important in determining the stringency of the hybridization process, with more stringent conditions allowing less non-specific binding, i.e., binding between pairs of nucleic acid strands that are not perfectly matched. Permissive conditions for annealing of nucleic acid sequences are routinely determinable by one of ordinary skill in the art and may be consistent among hybridization experiments, whereas wash conditions may be varied among experiments to achieve the desired stringency, and therefore hybridization specificity. Permissive annealing conditions occur, for example, at 68°C in the presence of about 6 x SSC, about 1% (w/v) SDS, and about 100 µg/ml denatured salmon sperm DNA.

Generally, stringency of hybridization is expressed, in part, with reference to the temperature under which the wash step is carried out. Generally, such wash temperatures are selected to be about 5°C to 20°C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength and pH. The T_m is the temperature (under defined ionic strength and pH) at which 50% of the target sequence hybridizes to a perfectly matched probe. An equation for calculating T_m and conditions for nucleic acid hybridization are well known and can be found in Sambrook et al., 1989, Molecular Cloning: A Laboratory Manual, 2nd ed., vol. 1-3, Cold Spring Harbor Press, Plainview NY; specifically see volume 2, chapter 9.

High stringency conditions for hybridization between polynucleotides of the present invention include wash conditions of 68°C in the presence of about 0.2 x SSC and about 0.1% SDS, for 1 hour. Alternatively, temperatures of about 65°C, 60°C, 55°C, or 42°C may be used. SSC concentration may be varied from about 0.1 to 2 x SSC, with SDS being present at about 0.1%. Typically, blocking reagents are used to block non-specific hybridization. Such blocking reagents include, for instance, denatured salmon sperm DNA at about 100-200 µg/ml. Organic solvent, such as formamide at a concentration of about 35-50% v/v, may also be used under particular circumstances, such as for RNA:DNA hybridizations. Useful variations on these wash conditions will be readily apparent to those of ordinary skill in the art. Hybridization, particularly under high stringency conditions, may be suggestive of evolutionary similarity between the nucleotides. Such similarity is strongly indicative of a similar role for the nucleotides and their encoded polypeptides.

The term "hybridization complex" refers to a complex formed between two nucleic acid sequences by virtue of the formation of hydrogen bonds between complementary bases. A hybridization complex may be formed in solution (e.g., C_0t or R_0t analysis) or formed between one nucleic acid sequence present in solution and another nucleic acid sequence immobilized on a solid support (e.g., paper, membranes, filters, chips, pins or glass slides, or any other appropriate substrate to which cells or their nucleic acids have been fixed).

The words "insertion" and "addition" refer to changes in an amino acid or nucleotide

sequence resulting in the addition of one or more amino acid residues or nucleotides, respectively.

"Immune response" can refer to conditions associated with inflammation, trauma, immune disorders, or infectious or genetic disease, etc. These conditions can be characterized by expression of various factors, e.g., cytokines, chemokines, and other signaling molecules, which may affect cellular and systemic defense systems.

The term "microarray" refers to an arrangement of distinct polynucleotides on a substrate.

The terms "element" and "array element" in a microarray context, refer to hybridizable polynucleotides arranged on the surface of a substrate.

The term "modulate" refers to a change in the activity of NuABP. For example, modulation may cause an increase or a decrease in protein activity, binding characteristics, or any other biological, functional, or immunological properties of NuABP.

The phrases "nucleic acid" and "nucleic acid sequence" refer to a nucleotide, oligonucleotide, polynucleotide, or any fragment thereof. These phrases also refer to DNA or RNA of genomic or synthetic origin which may be single-stranded or double-stranded and may represent the sense or the antisense strand, to peptide nucleic acid (PNA), or to any DNA-like or RNA-like material.

"Operably linked" refers to the situation in which a first nucleic acid sequence is placed in a functional relationship with the second nucleic acid sequence. For instance, a promoter is operably linked to a coding sequence if the promoter affects the transcription or expression of the coding sequence. Generally, operably linked DNA sequences may be in close proximity or contiguous and, where necessary to join two protein coding regions, in the same reading frame.

"Peptide nucleic acid" (PNA) refers to an antisense molecule or anti-gene agent which comprises an oligonucleotide of at least about 5 nucleotides in length linked to a peptide backbone of amino acid residues ending in lysine. The terminal lysine confers solubility to the composition. PNAs preferentially bind complementary single stranded DNA or RNA and stop transcript elongation, and may be pegylated to extend their lifespan in the cell.

"Probe" refers to nucleic acid sequences encoding NuABP, their complements, or fragments thereof, which are used to detect identical, allelic or related nucleic acid sequences. Probes are isolated oligonucleotides or polynucleotides attached to a detectable label or reporter molecule. Typical labels include radioactive isotopes, ligands, chemiluminescent agents, and enzymes.

"Primers" are short nucleic acids, usually DNA oligonucleotides, which may be annealed to a target polynucleotide by complementary base-pairing. The primer may then be extended along the target DNA strand by a DNA polymerase enzyme. Primer pairs can be used for amplification (and identification) of a nucleic acid sequence, e.g., by the polymerase chain reaction (PCR).

Probes and primers as used in the present invention typically comprise at least 15 contiguous nucleotides of a known sequence. In order to enhance specificity, longer probes and primers may also

be employed, such as probes and primers that comprise at least 20, 25, 30, 40, 50, 60, 70, 80, 90, 100, or at least 150 consecutive nucleotides of the disclosed nucleic acid sequences. Probes and primers may be considerably longer than these examples, and it is understood that any length supported by the specification, including the tables, figures, and Sequence Listing, may be used.

5 Methods for preparing and using probes and primers are described in the references, for example Sambrook et al., 1989, Molecular Cloning: A Laboratory Manual, 2nd ed., vol. 1-3, Cold Spring Harbor Press, Plainview NY; Ausubel et al., 1987, Current Protocols in Molecular Biology, Greene Publ. Assoc. & Wiley-Intersciences, New York NY; Innis et al., 1990, PCR Protocols, A Guide to Methods and Applications, Academic Press, San Diego CA. PCR primer pairs can be
10 derived from a known sequence, for example, by using computer programs intended for that purpose such as Primer (Version 0.5, 1991, Whitehead Institute for Biomedical Research, Cambridge MA).

 Oligonucleotides for use as primers are selected using software known in the art for such purpose. For example, OLIGO 4.06 software is useful for the selection of PCR primer pairs of up to 100 nucleotides each, and for the analysis of oligonucleotides and larger polynucleotides of up to
15 5,000 nucleotides from an input polynucleotide sequence of up to 32 kilobases. Similar primer selection programs have incorporated additional features for expanded capabilities. For example, the PrimOU primer selection program (available to the public from the Genome Center at University of Texas South West Medical Center, Dallas TX) is capable of choosing specific primers from megabase sequences and is thus useful for designing primers on a genome-wide scope. The Primer3 primer
20 selection program (available to the public from the Whitehead Institute/MIT Center for Genome Research, Cambridge MA) allows the user to input a "mispriming library," in which sequences to avoid as primer binding sites are user-specified. Primer3 is useful, in particular, for the selection of oligonucleotides for microarrays. (The source code for the latter two primer selection programs may also be obtained from their respective sources and modified to meet the user's specific needs.) The
25 PrimeGen program (available to the public from the UK Human Genome Mapping Project Resource Centre, Cambridge UK) designs primers based on multiple sequence alignments, thereby allowing selection of primers that hybridize to either the most conserved or least conserved regions of aligned nucleic acid sequences. Hence, this program is useful for identification of both unique and conserved oligonucleotides and polynucleotide fragments. The oligonucleotides and polynucleotide fragments
30 identified by any of the above selection methods are useful in hybridization technologies, for example, as PCR or sequencing primers, microarray elements, or specific probes to identify fully or partially complementary polynucleotides in a sample of nucleic acids. Methods of oligonucleotide selection are not limited to those described above.

 A "recombinant nucleic acid" is a sequence that is not naturally occurring or has a sequence
35 that is made by an artificial combination of two or more otherwise separated segments of sequence.

This artificial combination is often accomplished by chemical synthesis or, more commonly, by the artificial manipulation of isolated segments of nucleic acids, e.g., by genetic engineering techniques such as those described in Sambrook, supra. The term recombinant includes nucleic acids that have been altered solely by addition, substitution, or deletion of a portion of the nucleic acid. Frequently, a
5 recombinant nucleic acid may include a nucleic acid sequence operably linked to a promoter sequence. Such a recombinant nucleic acid may be part of a vector that is used, for example, to transform a cell.

Alternatively, such recombinant nucleic acids may be part of a viral vector, e.g., based on a vaccinia virus, that could be use to vaccinate a mammal wherein the recombinant nucleic acid is
10 expressed, inducing a protective immunological response in the mammal.

The term "sample" is used in its broadest sense. A sample suspected of containing nucleic acids encoding NuABP, or fragments thereof, or NuABP itself, may comprise a bodily fluid; an extract from a cell, chromosome, organelle, or membrane isolated from a cell; a cell; genomic DNA, RNA, or cDNA, in solution or bound to a substrate; a tissue; a tissue print; etc.

The terms "specific binding" and "specifically binding" refer to that interaction between a protein or peptide and an agonist, an antibody, an antagonist, a small molecule, or any natural or synthetic binding composition. The interaction is dependent upon the presence of a particular structure of the protein, e.g., the antigenic determinant or epitope, recognized by the binding molecule. For example, if an antibody is specific for epitope "A," the presence of a polypeptide
15 containing the epitope A, or the presence of free unlabeled A, in a reaction containing free labeled A and the antibody will reduce the amount of labeled A that binds to the antibody.

The term "substantially purified" refers to nucleic acid or amino acid sequences that are removed from their natural environment and are isolated or separated, and are at least 60% free, preferably at least 75% free, and most preferably at least 90% free from other components with which
25 they are naturally associated.

A "substitution" refers to the replacement of one or more amino acids or nucleotides by different amino acids or nucleotides, respectively.

"Substrate" refers to any suitable rigid or semi-rigid support including membranes, filters, chips, slides, wafers, fibers, magnetic or nonmagnetic beads, gels, tubing, plates, polymers,
30 microparticles and capillaries. The substrate can have a variety of surface forms, such as wells, trenches, pins, channels and pores, to which polynucleotides or polypeptides are bound.

"Transformation" describes a process by which exogenous DNA enters and changes a recipient cell. Transformation may occur under natural or artificial conditions according to various methods well known in the art, and may rely on any known method for the insertion of foreign nucleic
35 acid sequences into a prokaryotic or eukaryotic host cell. The method for transformation is selected

based on the type of host cell being transformed and may include, but is not limited to, viral infection, electroporation, heat shock, lipofection, and particle bombardment. The term "transformed" cells includes stably transformed cells in which the inserted DNA is capable of replication either as an autonomously replicating plasmid or as part of the host chromosome, as well as transiently

5 transformed cells which express the inserted DNA or RNA for limited periods of time.

A "variant" of a particular nucleic acid sequence is defined as a nucleic acid sequence having at least 40% sequence identity to the particular nucleic acid sequence over a certain length of one of the nucleic acid sequences using blastn with the "BLAST 2 Sequences" tool Version 2.0.9 (May-07-1999) set at default parameters. Such a pair of nucleic acids may show, for example, at least 50%, at
10 least 60%, at least 70%, at least 80%, at least 85%, at least 90%, at least 95% or at least 98% or greater sequence identity over a certain defined length. A variant may be described as, for example, an "allelic" (as defined above), "splice," "species," or "polymorphic" variant. A splice variant may have significant identity to a reference molecule, but will generally have a greater or lesser number of polynucleotides due to alternate splicing of exons during mRNA processing. The corresponding
15 polypeptide may possess additional functional domains or lack domains that are present in the reference molecule. Species variants are polynucleotide sequences that vary from one species to another. The resulting polypeptides generally will have significant amino acid identity relative to each other. A polymorphic variant is a variation in the polynucleotide sequence of a particular gene between individuals of a given species. Polymorphic variants also may encompass "single nucleotide
20 polymorphisms" (SNPs) in which the polynucleotide sequence varies by one nucleotide base. The presence of SNPs may be indicative of, for example, a certain population, a disease state, or a propensity for a disease state.

A "variant" of a particular polypeptide sequence is defined as a polypeptide sequence having at least 40% sequence identity to the particular polypeptide sequence over a certain length of one of
25 the polypeptide sequences using blastp with the "BLAST 2 Sequences" tool Version 2.0.9 (May-07-1999) set at default parameters. Such a pair of polypeptides may show, for example, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, or at least 98% or greater sequence identity over a certain defined length of one of the polypeptides.

30 THE INVENTION

The invention is based on the discovery of new human nucleic-acid binding proteins (NuABP), the polynucleotides encoding NuABP, and the use of these compositions for the diagnosis, treatment, or prevention of reproductive, immune, and neurological disorders, and cell proliferative disorders including cancer.

35 Table 1 lists the Incyte clones used to assemble full length nucleotide sequences encoding

NuABP. Columns 1 and 2 show the sequence identification numbers (SEQ ID NOs) of the polypeptide and nucleotide sequences, respectively. Column 3 shows the clone IDs of the Incyte clones in which nucleic acids encoding each NuABP were identified, and column 4 shows the cDNA libraries from which these clones were isolated. Column 5 shows Incyte clones and their
 5 corresponding cDNA libraries. Clones for which cDNA libraries are not indicated were derived from pooled cDNA libraries. The Incyte clones in column 5 were used to assemble the consensus nucleotide sequence of each NuABP and are useful as fragments in hybridization technologies.

The columns of Table 2 show various properties of each of the polypeptides of the invention: column 1 references the SEQ ID NO; column 2 shows the number of amino acid residues in each
 10 polypeptide; column 3 shows potential phosphorylation sites; column 4 shows potential glycosylation sites; column 5 shows the amino acid residues comprising signature sequences and motifs; column 6 shows identification or homologous sequences as identified by BLAST analysis; and column 7 shows analytical methods and in some cases, searchable databases to which the analytical methods were applied. The methods of column 7 were used to characterize each polypeptide through sequence
 15 homology and protein motifs.

The columns of Table 3 show the tissue-specificity and diseases, disorders, or conditions associated with nucleotide sequences encoding NuABP. The first column of Table 3 lists the nucleotide SEQ ID NOs. Column 2 lists fragments of the nucleotide sequences of column 1. These fragments are useful, for example, in hybridization or amplification technologies to identify SEQ ID
 20 NO:56-110 and to distinguish between SEQ ID NO:56-110 and related polynucleotide sequences. The polypeptides encoded by these fragments are useful, for example, as immunogenic peptides. Column 3 lists tissue categories which express NuABP as a fraction of total tissues expressing NuABP. Column 4 lists diseases, disorders, or conditions associated with those tissues expressing NuABP as a fraction of total tissues expressing NuABP. Of particular note is the expression of SEQ
 25 ID NO:83 and SEQ ID NO:110 in neurological tissue. About 53% of the cDNA libraries expressing SEQ ID NO:83 are derived from neurological tissue. Furthermore, SEQ ID NO:110 expression is detected exclusively in a cDNA library derived from brain tissue afflicted with Huntington's disease. Column 5 lists the vectors used to subclone each cDNA library.

The columns of Table 4 show descriptions of the tissues used to construct the cDNA libraries
 30 from which cDNA clones encoding NuABP were isolated. Column 1 references the nucleotide SEQ ID NOs, column 2 shows the cDNA libraries from which these clones were isolated, and column 3 shows the tissue origins and other descriptive information relevant to the cDNA libraries in column 2.

Fragments of the nucleotide sequences encoding NuABP are useful, for example, in hybridization or amplification technologies to identify SEQ ID NOS:56-110 and to distinguish
 35 between SEQ ID NOS:56-110 and related polynucleotide sequences. The polypeptides encoded by

these fragments are useful, for example, as immunogenic peptides.

The invention also encompasses NuABP variants. A preferred NuABP variant is one which has at least about 80%, or alternatively at least about 90%, or even at least about 95% amino acid sequence identity to the NuABP amino acid sequence, and which contains at least one functional or structural characteristic of NuABP.

The invention also encompasses polynucleotides which encode NuABP. In a particular embodiment, the invention encompasses a polynucleotide sequence comprising a sequence selected from the group consisting of SEQ ID NO:56-110, which encodes NuABP.

The invention also encompasses a variant of a polynucleotide sequence encoding NuABP. In particular, such a variant polynucleotide sequence will have at least about 70%, or alternatively at least about 85%, or even at least about 95% polynucleotide sequence identity to the polynucleotide sequence encoding NuABP. A particular aspect of the invention encompasses a variant of a polynucleotide sequence comprising a sequence selected from the group consisting of SEQ ID NO:56-110 which has at least about 70%, or alternatively at least about 85%, or even at least about 95% polynucleotide sequence identity to a nucleic acid sequence selected from the group consisting of SEQ ID NO:56-110. Any one of the polynucleotide variants described above can encode an amino acid sequence which contains at least one functional or structural characteristic of NuABP.

It will be appreciated by those skilled in the art that as a result of the degeneracy of the genetic code, a multitude of polynucleotide sequences encoding NuABP, some bearing minimal similarity to the polynucleotide sequences of any known and naturally occurring gene, may be produced. Thus, the invention contemplates each and every possible variation of polynucleotide sequence that could be made by selecting combinations based on possible codon choices. These combinations are made in accordance with the standard triplet genetic code as applied to the polynucleotide sequence of naturally occurring NuABP, and all such variations are to be considered as being specifically disclosed.

Although nucleotide sequences which encode NuABP and its variants are generally capable of hybridizing to the nucleotide sequence of the naturally occurring NuABP under appropriately selected conditions of stringency, it may be advantageous to produce nucleotide sequences encoding NuABP or its derivatives possessing a substantially different codon usage, e.g., inclusion of non-naturally occurring codons. Codons may be selected to increase the rate at which expression of the peptide occurs in a particular prokaryotic or eukaryotic host in accordance with the frequency with which particular codons are utilized by the host. Other reasons for substantially altering the nucleotide sequence encoding NuABP and its derivatives without altering the encoded amino acid sequences include the production of RNA transcripts having more desirable properties, such as a greater half-life, than transcripts produced from the naturally occurring sequence.

The invention also encompasses production of DNA sequences which encode NuABP and NuABP derivatives, or fragments thereof, entirely by synthetic chemistry. After production, the synthetic sequence may be inserted into any of the many available expression vectors and cell systems using reagents well known in the art. Moreover, synthetic chemistry may be used to introduce
5 mutations into a sequence encoding NuABP or any fragment thereof.

Also encompassed by the invention are polynucleotide sequences that are capable of hybridizing to the claimed polynucleotide sequences, and, in particular, to those shown in SEQ ID NO:56-110 and fragments thereof under various conditions of stringency. (See, e.g., Wahl, G.M. and S.L. Berger (1987) *Methods Enzymol.* 152:399-407; Kimmel, A.R. (1987) *Methods Enzymol.*
10 152:507-511.) Hybridization conditions, including annealing and wash conditions, are described in "Definitions."

Methods for DNA sequencing are well known in the art and may be used to practice any of the embodiments of the invention. The methods may employ such enzymes as the Klenow fragment of DNA polymerase I, SEQUENASE (US Biochemical, Cleveland OH), Taq polymerase (Perkin-
15 Elmer), thermostable T7 polymerase (Amersham Pharmacia Biotech, Piscataway NJ), or combinations of polymerases and proofreading exonucleases such as those found in the ELONGASE amplification system (Life Technologies, Gaithersburg MD). Preferably, sequence preparation is automated with machines such as the MICROLAB 2200 liquid transfer system (Hamilton, Reno NV), PTC200 thermal cycler (MJ Research, Watertown MA) and ABI CATALYST 800 thermal cycler
20 (Perkin-Elmer). Sequencing is then carried out using either the ABI 373 or 377 DNA sequencing system (Perkin-Elmer), the MEGABACE 1000 DNA sequencing system (Molecular Dynamics, Sunnyvale CA), or other systems known in the art. The resulting sequences are analyzed using a variety of algorithms which are well known in the art. (See, e.g., Ausubel, F.M. (1997) Short Protocols in Molecular Biology, John Wiley & Sons, New York NY, unit 7.7; Meyers, R.A. (1995)
25 Molecular Biology and Biotechnology, Wiley VCH, New York NY, pp. 856-853.)

The nucleic acid sequences encoding NuABP may be extended utilizing a partial nucleotide sequence and employing various PCR-based methods known in the art to detect upstream sequences, such as promoters and regulatory elements. For example, one method which may be employed, restriction-site PCR, uses universal and nested primers to amplify unknown sequence from genomic
30 DNA within a cloning vector. (See, e.g., Sarkar, G. (1993) *PCR Methods Applic.* 2:318-322.) Another method, inverse PCR, uses primers that extend in divergent directions to amplify unknown sequence from a circularized template. The template is derived from restriction fragments comprising a known genomic locus and surrounding sequences. (See, e.g., Triglia, T. et al. (1988) *Nucleic Acids Res.* 16:8186.) A third method, capture PCR, involves PCR amplification of DNA fragments adjacent
35 to known sequences in human and yeast artificial chromosome DNA. (See, e.g., Lagerstrom, M. et al.

(1991) PCR Methods Applic. 1:111-119.) In this method, multiple restriction enzyme digestions and ligations may be used to insert an engineered double-stranded sequence into a region of unknown sequence before performing PCR. Other methods which may be used to retrieve unknown sequences are known in the art. (See, e.g., Parker, J.D. et al. (1991) Nucleic Acids Res. 19:3055-3060).

- 5 Additionally, one may use PCR, nested primers, and PROMOTERFINDER libraries (Clontech, Palo Alto CA) to walk genomic DNA. This procedure avoids the need to screen libraries and is useful in finding intron/exon junctions. For all PCR-based methods, primers may be designed using commercially available software, such as OLIGO 4.06 Primer Analysis software (National Biosciences, Plymouth MN) or another appropriate program, to be about 22 to 30 nucleotides in
10 length, to have a GC content of about 50% or more, and to anneal to the template at temperatures of about 68°C to 72°C.

- When screening for full-length cDNAs, it is preferable to use libraries that have been size-selected to include larger cDNAs. In addition, random-primed libraries, which often include sequences containing the 5' regions of genes, are preferable for situations in which an oligo d(T)
15 library does not yield a full-length cDNA. Genomic libraries may be useful for extension of sequence into 5' non-transcribed regulatory regions.

- Capillary electrophoresis systems which are commercially available may be used to analyze the size or confirm the nucleotide sequence of sequencing or PCR products. In particular, capillary sequencing may employ flowable polymers for electrophoretic separation, four different nucleotide-
20 specific, laser-stimulated fluorescent dyes, and a charge coupled device camera for detection of the emitted wavelengths. Output/light intensity may be converted to electrical signal using appropriate software (e.g., GENOTYPER and SEQUENCE NAVIGATOR, Perkin-Elmer), and the entire process from loading of samples to computer analysis and electronic data display may be computer controlled. Capillary electrophoresis is especially preferable for sequencing small DNA fragments which may be
25 present in limited amounts in a particular sample.

- In another embodiment of the invention, polynucleotide sequences or fragments thereof which encode NuABP may be cloned in recombinant DNA molecules that direct expression of NuABP, or fragments or functional equivalents thereof, in appropriate host cells. Due to the inherent degeneracy of the genetic code, other DNA sequences which encode substantially the same or a
30 functionally equivalent amino acid sequence may be produced and used to express NuABP.

- The nucleotide sequences of the present invention can be engineered using methods generally known in the art in order to alter NuABP-encoding sequences for a variety of purposes including, but not limited to, modification of the cloning, processing, and/or expression of the gene product. DNA shuffling by random fragmentation and PCR reassembly of gene fragments and synthetic
35 oligonucleotides may be used to engineer the nucleotide sequences. For example, oligonucleotide-

mediated site-directed mutagenesis may be used to introduce mutations that create new restriction sites, alter glycosylation patterns, change codon preference, produce splice variants, and so forth.

In another embodiment, sequences encoding NuABP may be synthesized, in whole or in part, using chemical methods well known in the art. (See, e.g., Caruthers, M.H. et al. (1980) Nucleic Acids Symp. Ser. 7:215-223; and Horn, T. et al. (1980) Nucleic Acids Symp. Ser. 7:225-232.)

Alternatively, NuABP itself or a fragment thereof may be synthesized using chemical methods. For example, peptide synthesis can be performed using various solid-phase techniques. (See, e.g., Roberge, J.Y. et al. (1995) Science 269:202-204.) Automated synthesis may be achieved using the ABI 431A peptide synthesizer (Perkin-Elmer). Additionally, the amino acid sequence of NuABP, or any part thereof, may be altered during direct synthesis and/or combined with sequences from other proteins, or any part thereof, to produce a variant polypeptide.

The peptide may be substantially purified by preparative high performance liquid chromatography. (See, e.g., Chiez, R.M. and F.Z. Regnier (1990) Methods Enzymol. 182:392-421.) The composition of the synthetic peptides may be confirmed by amino acid analysis or by sequencing. (See, e.g., Creighton, T. (1984) Proteins, Structures and Molecular Properties, WH Freeman, New York NY.)

In order to express a biologically active NuABP, the nucleotide sequences encoding NuABP or derivatives thereof may be inserted into an appropriate expression vector, i.e., a vector which contains the necessary elements for transcriptional and translational control of the inserted coding sequence in a suitable host. These elements include regulatory sequences, such as enhancers, constitutive and inducible promoters, and 5' and 3' untranslated regions in the vector and in polynucleotide sequences encoding NuABP. Such elements may vary in their strength and specificity. Specific initiation signals may also be used to achieve more efficient translation of sequences encoding NuABP. Such signals include the ATG initiation codon and adjacent sequences, e.g. the Kozak sequence. In cases where sequences encoding NuABP and its initiation codon and upstream regulatory sequences are inserted into the appropriate expression vector, no additional transcriptional or translational control signals may be needed. However, in cases where only coding sequence, or a fragment thereof, is inserted, exogenous translational control signals including an in-frame ATG initiation codon should be provided by the vector. Exogenous translational elements and initiation codons may be of various origins, both natural and synthetic. The efficiency of expression may be enhanced by the inclusion of enhancers appropriate for the particular host cell system used. (See, e.g., Scharf, D. et al. (1994) Results Probl. Cell Differ. 20:125-162.)

Methods which are well known to those skilled in the art may be used to construct expression vectors containing sequences encoding NuABP and appropriate transcriptional and translational control elements. These methods include in vitro recombinant DNA techniques, synthetic techniques,

and in vivo genetic recombination. (See, e.g., Sambrook, J. et al. (1989) Molecular Cloning, A Laboratory Manual, Cold Spring Harbor Press, Plainview NY, ch. 4, 8, and 16-17; Ausubel, F.M. et al. (1995) Current Protocols in Molecular Biology, John Wiley & Sons, New York NY, ch. 9, 13, and 16.)

5 A variety of expression vector/host systems may be utilized to contain and express sequences encoding NuABP. These include, but are not limited to, microorganisms such as bacteria transformed with recombinant bacteriophage, plasmid, or cosmid DNA expression vectors; yeast transformed with yeast expression vectors; insect cell systems infected with viral expression vectors (e.g., baculovirus); plant cell systems transformed with viral expression vectors (e.g., cauliflower mosaic virus, CaMV, or
10 tobacco mosaic virus, TMV) or with bacterial expression vectors (e.g., Ti or pBR322 plasmids); or animal cell systems. The invention is not limited by the host cell employed.

In bacterial systems, a number of cloning and expression vectors may be selected depending upon the use intended for polynucleotide sequences encoding NuABP. For example, routine cloning, subcloning, and propagation of polynucleotide sequences encoding NuABP can be achieved using a
15 multifunctional E. coli vector such as PBLUESCRIPT (Stratagene, La Jolla CA) or PSPORT1 plasmid (Life Technologies). Ligation of sequences encoding NuABP into the vector's multiple cloning site disrupts the *lacZ* gene, allowing a colorimetric screening procedure for identification of transformed bacteria containing recombinant molecules. In addition, these vectors may be useful for
20 in vitro transcription, dideoxy sequencing, single strand rescue with helper phage, and creation of nested deletions in the cloned sequence. (See, e.g., Van Heeke, G. and S.M. Schuster (1989) J. Biol. Chem. 264:5503-5509.) When large quantities of NuABP are needed, e.g. for the production of antibodies, vectors which direct high level expression of NuABP may be used. For example, vectors containing the strong, inducible T5 or T7 bacteriophage promoter may be used.

Yeast expression systems may be used for production of NuABP. A number of vectors
25 containing constitutive or inducible promoters, such as alpha factor, alcohol oxidase, and PGH promoters, may be used in the yeast Saccharomyces cerevisiae or Pichia pastoris. In addition, such vectors direct either the secretion or intracellular retention of expressed proteins and enable integration of foreign sequences into the host genome for stable propagation. (See, e.g., Ausubel, 1995, supra; Bitter, G.A. et al. (1987) Methods Enzymol. 153:516-544; and Scorer, C.A. et al. (1994)
30 Bio/Technology 12:181-184.)

Plant systems may also be used for expression of NuABP. Transcription of sequences encoding NuABP may be driven viral promoters, e.g., the 35S and 19S promoters of CaMV used alone or in combination with the omega leader sequence from TMV (Takamatsu, N. (1987) EMBO J. 6:307-311). Alternatively, plant promoters such as the small subunit of RUBISCO or heat shock
35 promoters may be used. (See, e.g., Coruzzi, G. et al. (1984) EMBO J. 3:1671-1680; Broglie, R. et al.

(1984) Science 224:838-843; and Winter, J. et al. (1991) Results Probl. Cell Differ. 17:85-105.)

These constructs can be introduced into plant cells by direct DNA transformation or pathogen-mediated transfection. (See, e.g., The McGraw Hill Yearbook of Science and Technology (1992) McGraw Hill, New York NY, pp. 191-196.)

5 In mammalian cells, a number of viral-based expression systems may be utilized. In cases where an adenovirus is used as an expression vector, sequences encoding NuABP may be ligated into an adenovirus transcription/translation complex consisting of the late promoter and tripartite leader sequence. Insertion in a non-essential E1 or E3 region of the viral genome may be used to obtain infective virus which expresses NuABP in host cells. (See, e.g., Logan, J. and T. Shenk (1984) Proc.
10 Natl. Acad. Sci. USA 81:3655-3659.) In addition, transcription enhancers, such as the Rous sarcoma virus (RSV) enhancer, may be used to increase expression in mammalian host cells. SV40 or EBV-based vectors may also be used for high-level protein expression.

Human artificial chromosomes (HACs) may also be employed to deliver larger fragments of DNA than can be contained in and expressed from a plasmid. HACs of about 6 kb to 10 Mb are
15 constructed and delivered via conventional delivery methods (liposomes, polycationic amino polymers, or vesicles) for therapeutic purposes. (See, e.g., Harrington, J.J. et al. (1997) Nat. Genet. 15:345-355.)

For long term production of recombinant proteins in mammalian systems, stable expression of NuABP in cell lines is preferred. For example, sequences encoding NuABP can be transformed into
20 cell lines using expression vectors which may contain viral origins of replication and/or endogenous expression elements and a selectable marker gene on the same or on a separate vector. Following the introduction of the vector, cells may be allowed to grow for about 1 to 2 days in enriched media before being switched to selective media. The purpose of the selectable marker is to confer resistance to a selective agent, and its presence allows growth and recovery of cells which successfully express
25 the introduced sequences. Resistant clones of stably transformed cells may be propagated using tissue culture techniques appropriate to the cell type.

Any number of selection systems may be used to recover transformed cell lines. These include, but are not limited to, the herpes simplex virus thymidine kinase and adenine phosphoribosyltransferase genes, for use in *tk* and *apr* cells, respectively. (See, e.g., Wigler, M. et
30 al. (1977) Cell 11:223-232; Lowy, I. et al. (1980) Cell 22:817-823.) Also, antimetabolite, antibiotic, or herbicide resistance can be used as the basis for selection. For example, *dhfr* confers resistance to methotrexate; *neo* confers resistance to the aminoglycosides neomycin and G-418; and *als* and *pat* confer resistance to chlorsulfuron and phosphinotricin acetyltransferase, respectively. (See, e.g.,
Wigler, M. et al. (1980) Proc. Natl. Acad. Sci. USA 77:3567-3570; Colbere-Garapin, F. et al. (1981)
35 J. Mol. Biol. 150:1-14.) Additional selectable genes have been described, e.g., *trpB* and *hisD*, which

alter cellular requirements for metabolites. (See, e.g., Hartman, S.C. and R.C. Mulligan (1988) Proc. Natl. Acad. Sci. USA 85:8047-8051.) Visible markers, e.g., anthocyanins, green fluorescent proteins (GFP: Clontech), β glucuronidase and its substrate β -glucuronide, or luciferase and its substrate luciferin may be used. These markers can be used not only to identify transformants, but also to

5 quantify the amount of transient or stable protein expression attributable to a specific vector system. (See, e.g., Rhodes, C.A. (1995) Methods Mol. Biol. 55:121-131.)

Although the presence/absence of marker gene expression suggests that the gene of interest is also present, the presence and expression of the gene may need to be confirmed. For example, if the sequence encoding NuABP is inserted within a marker gene sequence, transformed cells containing

10 sequences encoding NuABP can be identified by the absence of marker gene function. Alternatively, a marker gene can be placed in tandem with a sequence encoding NuABP under the control of a single promoter. Expression of the marker gene in response to induction or selection usually indicates expression of the tandem gene as well.

In general, host cells that contain the nucleic acid sequence encoding NuABP and that express

15 NuABP may be identified by a variety of procedures known to those of skill in the art. These procedures include, but are not limited to, DNA-DNA or DNA-RNA hybridizations, PCR amplification, and protein bioassay or immunoassay techniques which include membrane, solution, or chip based technologies for the detection and/or quantification of nucleic acid or protein sequences.

Immunological methods for detecting and measuring the expression of NuABP using either

20 specific polyclonal or monoclonal antibodies are known in the art. Examples of such techniques include enzyme-linked immunosorbent assays (ELISAs), radioimmunoassays (RIAs), and fluorescence activated cell sorting (FACS). A two-site, monoclonal-based immunoassay utilizing monoclonal antibodies reactive to two non-interfering epitopes on NuABP is preferred, but a competitive binding assay may be employed. These and other assays are well known in the art. (See,

25 e.g., Hampton, R. et al. (1990) Serological Methods, a Laboratory Manual, APS Press, St. Paul MN, Sect. IV; Coligan, J.E. et al. (1997) Current Protocols in Immunology, Greene Pub. Associates and Wiley-Interscience, New York NY; and Pound, J.D. (1998) Immunochemical Protocols, Humana Press, Totowa NJ.)

A wide variety of labels and conjugation techniques are known by those skilled in the art and

30 may be used in various nucleic acid and amino acid assays. Means for producing labeled hybridization or PCR probes for detecting sequences related to polynucleotides encoding NuABP include oligolabeling, nick translation, end-labeling, or PCR amplification using a labeled nucleotide. Alternatively, the sequences encoding NuABP, or any fragments thereof, may be cloned into a vector for the production of an mRNA probe. Such vectors are known in the art, are commercially available,

35 and may be used to synthesize RNA probes in vitro by addition of an appropriate RNA polymerase

such as T7, T3, or SP6 and labeled nucleotides. These procedures may be conducted using a variety of commercially available kits, such as those provided by Amersham Pharmacia Biotech, Promega (Madison WI), and US Biochemical. Suitable reporter molecules or labels which may be used for ease of detection include radionuclides, enzymes, fluorescent, chemiluminescent, or chromogenic agents, as well as substrates, cofactors, inhibitors, magnetic particles, and the like.

Host cells transformed with nucleotide sequences encoding NuABP may be cultured under conditions suitable for the expression and recovery of the protein from cell culture. The protein produced by a transformed cell may be secreted or retained intracellularly depending on the sequence and/or the vector used. As will be understood by those of skill in the art, expression vectors containing polynucleotides which encode NuABP may be designed to contain signal sequences which direct secretion of NuABP through a prokaryotic or eukaryotic cell membrane.

In addition, a host cell strain may be chosen for its ability to modulate expression of the inserted sequences or to process the expressed protein in the desired fashion. Such modifications of the polypeptide include, but are not limited to, acetylation, carboxylation, glycosylation, phosphorylation, lipidation, and acylation. Post-translational processing which cleaves a "prepro" or "pro" form of the protein may also be used to specify protein targeting, folding, and/or activity. Different host cells which have specific cellular machinery and characteristic mechanisms for post-translational activities (e.g., CHO, HeLa, MDCK, HEK293, and WI38) are available from the American Type Culture Collection (ATCC, Manassas VA) and may be chosen to ensure the correct modification and processing of the foreign protein.

In another embodiment of the invention, natural, modified, or recombinant nucleic acid sequences encoding NuABP may be ligated to a heterologous sequence resulting in translation of a fusion protein in any of the aforementioned host systems. For example, a chimeric NuABP protein containing a heterologous moiety that can be recognized by a commercially available antibody may facilitate the screening of peptide libraries for inhibitors of NuABP activity. Heterologous protein and peptide moieties may also facilitate purification of fusion proteins using commercially available affinity matrices. Such moieties include, but are not limited to, glutathione S-transferase (GST), maltose binding protein (MBP), thioredoxin (Trx), calmodulin binding peptide (CBP), 6-His, FLAG, *c-myc*, and hemagglutinin (HA). GST, MBP, Trx, CBP, and 6-His enable purification of their cognate fusion proteins on immobilized glutathione, maltose, phenylarsine oxide, calmodulin, and metal-chelate resins, respectively. FLAG, *c-myc*, and hemagglutinin (HA) enable immunoaffinity purification of fusion proteins using commercially available monoclonal and polyclonal antibodies that specifically recognize these epitope tags. A fusion protein may also be engineered to contain a proteolytic cleavage site located between the NuABP encoding sequence and the heterologous protein sequence, so that NuABP may be cleaved away from the heterologous moiety following purification.

Methods for fusion protein expression and purification are discussed in Ausubel (1995, supra, ch. 10). A variety of commercially available kits may also be used to facilitate expression and purification of fusion proteins.

In a further embodiment of the invention, synthesis of radiolabeled NuABP may be achieved
5 in vitro using the TNT rabbit reticulocyte lysate or wheat germ extract system (Promega). These systems couple transcription and translation of protein-coding sequences operably associated with the T7, T3, or SP6 promoters. Translation takes place in the presence of a radiolabeled amino acid precursor, for example, ³⁵S-methionine.

Fragments of NuABP may be produced not only by recombinant means, but also by direct
10 peptide synthesis using solid-phase techniques. (See, e.g., Creighton, supra, pp. 55-60.) Protein synthesis may be performed by manual techniques or by automation. Automated synthesis may be achieved, for example, using the ABI 431A peptide synthesizer (Perkin-Elmer). Various fragments of NuABP may be synthesized separately and then combined to produce the full length molecule.

THERAPEUTICS

15 Chemical and structural similarity, e.g., in the context of sequences and motifs, exists between regions of NuABP and nucleic-acid binding proteins. In addition, the expression of NuABP is closely associated with proliferative, neuronal, inflamed, and cancerous tissues and tissues of the reproductive system. Therefore, NuABP appears to play a role in reproductive, immune, and neurological disorders, and cell proliferative disorders including cancer. In the treatment of disorders associated
20 with increased NuABP expression or activity, it is desirable to decrease the expression or activity of NuABP. In the treatment of disorders associated with decreased NuABP expression or activity, it is desirable to increase the expression or activity of NuABP.

Therefore, in one embodiment, NuABP or a fragment or derivative thereof may be administered to a subject to treat or prevent a disorder associated with decreased expression or activity
25 of NuABP. Examples of such disorders include, but are not limited to, a reproductive disorder such as disorders of prolactin production, infertility, including tubal disease, ovulatory defects, and endometriosis, disruptions of the estrous cycle, disruptions of the menstrual cycle, polycystic ovary syndrome, ovarian hyperstimulation syndrome, endometrial and ovarian tumors, uterine fibroids, autoimmune disorders, ectopic pregnancies, and teratogenesis; cancer of the breast, fibrocystic breast
30 disease, and galactorrhea; disruptions of spermatogenesis, abnormal sperm physiology, cancer of the testis, cancer of the prostate, benign prostatic hyperplasia, prostatitis, Peyronie's disease, impotence, carcinoma of the male breast, and gynecomastia; an immune disorder such as inflammation, actinic keratosis, acquired immunodeficiency syndrome (AIDS), Addison's disease, adult respiratory distress syndrome, allergies, ankylosing spondylitis, amyloidosis, anemia, arteriosclerosis, asthma,
35 atherosclerosis, autoimmune hemolytic anemia, autoimmune thyroiditis, bronchitis, bursitis,

cholecystitis, cirrhosis, contact dermatitis, Crohn's disease, atopic dermatitis, dermatomyositis, diabetes mellitus, emphysema, erythroblastosis fetalis, erythema nodosum, atrophic gastritis, glomerulonephritis, Goodpasture's syndrome, gout, Graves' disease, Hashimoto's thyroiditis, paroxysmal nocturnal hemoglobinuria, hepatitis, hypereosinophilia, irritable bowel syndrome,

5 episodic lymphopenia with lymphocytotoxins, mixed connective tissue disease (MCTD), multiple sclerosis, myasthenia gravis, myocardial or pericardial inflammation, myelofibrosis, osteoarthritis, osteoporosis, pancreatitis, polycythemia vera, polymyositis, psoriasis, Reiter's syndrome, rheumatoid arthritis, scleroderma, Sjögren's syndrome, systemic anaphylaxis, systemic lupus erythematosus, systemic sclerosis, primary thrombocythemia, thrombocytopenic purpura, ulcerative colitis, uveitis,

10 Werner syndrome, complications of cancer, hemodialysis, and extracorporeal circulation, trauma, and hematopoietic cancer including lymphoma, leukemia, and myeloma; a neurological disorder such as epilepsy, ischemic cerebrovascular disease, stroke, cerebral neoplasms, Alzheimer's disease, Pick's disease, Huntington's disease, dementia, Parkinson's disease and other extrapyramidal disorders, amyotrophic lateral sclerosis and other motor neuron disorders, progressive neural muscular atrophy,

15 retinitis pigmentosa, hereditary ataxias, multiple sclerosis and other demyelinating diseases, bacterial and viral meningitis, brain abscess, subdural empyema, epidural abscess, suppurative intracranial thrombophlebitis, myelitis and radiculitis, viral central nervous system disease, prion diseases including kuru, Creutzfeldt-Jakob disease, and Gerstmann-Straussler-Scheinker syndrome, fatal familial insomnia, nutritional and metabolic diseases of the nervous system, neurofibromatosis,

20 tuberous sclerosis, cerebelloretinal hemangioblastomatosis, encephalotrigeminal syndrome, mental retardation and other developmental disorders of the central nervous system, cerebral palsy, neuroskeletal disorders, autonomic nervous system disorders, cranial nerve disorders, spinal cord diseases, muscular dystrophy and other neuromuscular disorders, peripheral nervous system disorders, dermatomyositis and polymyositis, inherited, metabolic, endocrine, and toxic myopathies,

25 myasthenia gravis, periodic paralysis, mental disorders including mood, anxiety, and schizophrenic disorders, akathisia, amnesia, catatonia, diabetic neuropathy, tardive dyskinesia, dystonias, paranoid psychoses, postherpetic neuralgia, and Tourette's disorder; and a cell proliferative disorder such as actinic keratosis, arteriosclerosis, atherosclerosis, bursitis, cirrhosis, hepatitis, mixed connective tissue disease (MCTD), myelofibrosis, paroxysmal nocturnal hemoglobinuria, polycythemia vera, psoriasis,

30 primary thrombocythemia, and cancers including adenocarcinoma, leukemia, lymphoma, melanoma, myeloma, sarcoma, teratocarcinoma, and, in particular, cancers of the adrenal gland, bladder, bone, bone marrow, brain, breast, cervix, gall bladder, ganglia, gastrointestinal tract, heart, kidney, liver, lung, muscle, ovary, pancreas, parathyroid, penis, prostate, salivary glands, skin, spleen, testis, thymus, thyroid, and uterus.

35 In another embodiment, a vector capable of expressing NuABP or a fragment or derivative

thereof may be administered to a subject to treat or prevent a disorder associated with decreased expression or activity of NuABP including, but not limited to, those described above.

In a further embodiment, a pharmaceutical composition comprising a substantially purified NuABP in conjunction with a suitable pharmaceutical carrier may be administered to a subject to treat or prevent a disorder associated with decreased expression or activity of NuABP including, but not limited to, those provided above.

In still another embodiment, an agonist which modulates the activity of NuABP may be administered to a subject to treat or prevent a disorder associated with decreased expression or activity of NuABP including, but not limited to, those listed above.

In a further embodiment, an antagonist of NuABP may be administered to a subject to treat or prevent a disorder associated with increased expression or activity of NuABP. Examples of such disorders include, but are not limited to, those reproductive, immune, and neurological disorders, and cell proliferative disorders including cancer, described above. In one aspect, an antibody which specifically binds NuABP may be used directly as an antagonist or indirectly as a targeting or delivery mechanism for bringing a pharmaceutical agent to cells or tissues which express NuABP.

In an additional embodiment, a vector expressing the complement of the polynucleotide encoding NuABP may be administered to a subject to treat or prevent a disorder associated with increased expression or activity of NuABP including, but not limited to, those described above.

In other embodiments, any of the proteins, antagonists, antibodies, agonists, complementary sequences, or vectors of the invention may be administered in combination with other appropriate therapeutic agents. Selection of the appropriate agents for use in combination therapy may be made by one of ordinary skill in the art, according to conventional pharmaceutical principles. The combination of therapeutic agents may act synergistically to effect the treatment or prevention of the various disorders described above. Using this approach, one may be able to achieve therapeutic efficacy with lower dosages of each agent, thus reducing the potential for adverse side effects.

An antagonist of NuABP may be produced using methods which are generally known in the art. In particular, purified NuABP may be used to produce antibodies or to screen libraries of pharmaceutical agents to identify those which specifically bind NuABP. Antibodies to NuABP may also be generated using methods that are well known in the art. Such antibodies may include, but are not limited to, polyclonal, monoclonal, chimeric, and single chain antibodies, Fab fragments, and fragments produced by a Fab expression library. Neutralizing antibodies (i.e., those which inhibit dimer formation) are generally preferred for therapeutic use.

For the production of antibodies, various hosts including goats, rabbits, rats, mice, humans, and others may be immunized by injection with NuABP or with any fragment or oligopeptide thereof which has immunogenic properties. Depending on the host species, various adjuvants may be used to

increase immunological response. Such adjuvants include, but are not limited to, Freund's, mineral gels such as aluminum hydroxide, and surface active substances such as lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, KLH, and dinitrophenol. Among adjuvants used in humans, BCG (bacilli Calmette-Guerin) and Corynebacterium parvum are especially preferable.

5 It is preferred that the oligopeptides, peptides, or fragments used to induce antibodies to NuABP have an amino acid sequence consisting of at least about 5 amino acids, and generally will consist of at least about 10 amino acids. It is also preferable that these oligopeptides, peptides, or fragments are identical to a portion of the amino acid sequence of the natural protein and contain the entire amino acid sequence of a small, naturally occurring molecule. Short stretches of NuABP amino
10 acids may be fused with those of another protein, such as KLH, and antibodies to the chimeric molecule may be produced.

Monoclonal antibodies to NuABP may be prepared using any technique which provides for the production of antibody molecules by continuous cell lines in culture. These include, but are not limited to, the hybridoma technique, the human B-cell hybridoma technique, and the EBV-hybridoma
15 technique. (See, e.g., Kohler, G. et al. (1975) Nature 256:495-497; Kozbor, D. et al. (1985) J. Immunol. Methods 81:31-42; Cote, R.J. et al. (1983) Proc. Natl. Acad. Sci. USA 80:2026-2030; and Cole, S.P. et al. (1984) Mol. Cell Biol. 62:109-120.)

In addition, techniques developed for the production of "chimeric antibodies," such as the splicing of mouse antibody genes to human antibody genes to obtain a molecule with appropriate
20 antigen specificity and biological activity, can be used. (See, e.g., Morrison, S.L. et al. (1984) Proc. Natl. Acad. Sci. USA 81:6851-6855; Neuberger, M.S. et al. (1984) Nature 312:604-608; and Takeda, S. et al. (1985) Nature 314:452-454.) Alternatively, techniques described for the production of single chain antibodies may be adapted, using methods known in the art, to produce NuABP-specific single chain antibodies. Antibodies with related specificity, but of distinct idiotypic composition, may be
25 generated by chain shuffling from random combinatorial immunoglobulin libraries. (See, e.g., Burton, D.R. (1991) Proc. Natl. Acad. Sci. USA 88:10134-10137.)

Antibodies may also be produced by inducing in vivo production in the lymphocyte population or by screening immunoglobulin libraries or panels of highly specific binding reagents as disclosed in the literature. (See, e.g., Orlandi, R. et al. (1989) Proc. Natl. Acad. Sci. USA
30 86:3833-3837; Winter, G. et al. (1991) Nature 349:293-299.)

Antibody fragments which contain specific binding sites for NuABP may also be generated. For example, such fragments include, but are not limited to, F(ab')₂ fragments produced by pepsin digestion of the antibody molecule and Fab fragments generated by reducing the disulfide bridges of the F(ab')₂ fragments. Alternatively, Fab expression libraries may be constructed to allow rapid and
35 easy identification of monoclonal Fab fragments with the desired specificity. (See, e.g., Huse, W.D.

et al. (1989) Science 246:1275-1281.)

Various immunoassays may be used for screening to identify antibodies having the desired specificity. Numerous protocols for competitive binding or immunoradiometric assays using either polyclonal or monoclonal antibodies with established specificities are well known in the art. Such immunoassays typically involve the measurement of complex formation between NuABP and its specific antibody. A two-site, monoclonal-based immunoassay utilizing monoclonal antibodies reactive to two non-interfering NuABP epitopes is generally used, but a competitive binding assay may also be employed (Pound, supra).

Various methods such as Scatchard analysis in conjunction with radioimmunoassay techniques may be used to assess the affinity of antibodies for NuABP. Affinity is expressed as an association constant, K_a , which is defined as the molar concentration of NuABP-antibody complex divided by the molar concentrations of free antigen and free antibody under equilibrium conditions. The K_a determined for a preparation of polyclonal antibodies, which are heterogeneous in their affinities for multiple NuABP epitopes, represents the average affinity, or avidity, of the antibodies for NuABP. The K_a determined for a preparation of monoclonal antibodies, which are monospecific for a particular NuABP epitope, represents a true measure of affinity. High-affinity antibody preparations with K_a ranging from about 10^9 to 10^{12} L/mole are preferred for use in immunoassays in which the NuABP-antibody complex must withstand rigorous manipulations. Low-affinity antibody preparations with K_a ranging from about 10^6 to 10^7 L/mole are preferred for use in immunopurification and similar procedures which ultimately require dissociation of NuABP, preferably in active form, from the antibody (Catty, D. (1988) Antibodies, Volume I: A Practical Approach, IRL Press, Washington, DC; Liddell, J.E. and Cryer, A. (1991) A Practical Guide to Monoclonal Antibodies, John Wiley & Sons, New York NY).

The titer and avidity of polyclonal antibody preparations may be further evaluated to determine the quality and suitability of such preparations for certain downstream applications. For example, a polyclonal antibody preparation containing at least 1-2 mg specific antibody/ml, preferably 5-10 mg specific antibody/ml, is generally employed in procedures requiring precipitation of NuABP-antibody complexes. Procedures for evaluating antibody specificity, titer, and avidity, and guidelines for antibody quality and usage in various applications, are generally available. (See, e.g., Catty, supra, and Coligan et al. supra.)

In another embodiment of the invention, the polynucleotides encoding NuABP, or any fragment or complement thereof, may be used for therapeutic purposes. In one aspect, the complement of the polynucleotide encoding NuABP may be used in situations in which it would be desirable to block the transcription of the mRNA. In particular, cells may be transformed with sequences complementary to polynucleotides encoding NuABP. Thus, complementary molecules or

fragments may be used to modulate NuABP activity, or to achieve regulation of gene function. Such technology is now well known in the art, and sense or antisense oligonucleotides or larger fragments can be designed from various locations along the coding or control regions of sequences encoding NuABP.

5 Expression vectors derived from retroviruses, adenoviruses, or herpes or vaccinia viruses, or from various bacterial plasmids, may be used for delivery of nucleotide sequences to the targeted organ, tissue, or cell population. Methods which are well known to those skilled in the art can be used to construct vectors to express nucleic acid sequences complementary to the polynucleotides encoding NuABP. (See, e.g., Sambrook, supra; Ausubel, 1995, supra.)

10 Genes encoding NuABP can be turned off by transforming a cell or tissue with expression vectors which express high levels of a polynucleotide, or fragment thereof, encoding NuABP. Such constructs may be used to introduce untranslatable sense or antisense sequences into a cell. Even in the absence of integration into the DNA, such vectors may continue to transcribe RNA molecules until they are disabled by endogenous nucleases. Transient expression may last for a month or more
15 with a non-replicating vector, and may last even longer if appropriate replication elements are part of the vector system.

As mentioned above, modifications of gene expression can be obtained by designing complementary sequences or antisense molecules (DNA, RNA, or PNA) to the control, 5', or regulatory regions of the gene encoding NuABP. Oligonucleotides derived from the transcription
20 initiation site, e.g., between about positions -10 and +10 from the start site, may be employed. Similarly, inhibition can be achieved using triple helix base-pairing methodology. Triple helix pairing is useful because it causes inhibition of the ability of the double helix to open sufficiently for the binding of polymerases, transcription factors, or regulatory molecules. Recent therapeutic advances using triplex DNA have been described in the literature. (See, e.g., Gee, J.E. et al. (1994) in Huber,
25 B.E. and B.I. Carr, Molecular and Immunologic Approaches, Futura Publishing, Mt. Kisco NY, pp. 163-177.) A complementary sequence or antisense molecule may also be designed to block translation of mRNA by preventing the transcript from binding to ribosomes.

Ribozymes, enzymatic RNA molecules, may also be used to catalyze the specific cleavage of RNA. The mechanism of ribozyme action involves sequence-specific hybridization of the ribozyme
30 molecule to complementary target RNA, followed by endonucleolytic cleavage. For example, engineered hammerhead motif ribozyme molecules may specifically and efficiently catalyze endonucleolytic cleavage of sequences encoding NuABP.

Specific ribozyme cleavage sites within any potential RNA target are initially identified by scanning the target molecule for ribozyme cleavage sites, including the following sequences: GUA,
35 GUU, and GUC. Once identified, short RNA sequences of between 15 and 20 ribonucleotides,

corresponding to the region of the target gene containing the cleavage site, may be evaluated for secondary structural features which may render the oligonucleotide inoperable. The suitability of candidate targets may also be evaluated by testing accessibility to hybridization with complementary oligonucleotides using ribonuclease protection assays.

5 Complementary ribonucleic acid molecules and ribozymes of the invention may be prepared by any method known in the art for the synthesis of nucleic acid molecules. These include techniques for chemically synthesizing oligonucleotides such as solid phase phosphoramidite chemical synthesis. Alternatively, RNA molecules may be generated by in vitro and in vivo transcription of DNA sequences encoding NuABP. Such DNA sequences may be incorporated into a wide variety of
10 vectors with suitable RNA polymerase promoters such as T7 or SP6. Alternatively, these cDNA constructs that synthesize complementary RNA, constitutively or inducibly, can be introduced into cell lines, cells, or tissues.

RNA molecules may be modified to increase intracellular stability and half-life. Possible modifications include, but are not limited to, the addition of flanking sequences at the 5' and/or 3' ends
15 of the molecule, or the use of phosphorothioate or 2' O-methyl rather than phosphodiesterase linkages within the backbone of the molecule. This concept is inherent in the production of PNAs and can be extended in all of these molecules by the inclusion of nontraditional bases such as inosine, queosine, and wybutosine, as well as acetyl-, methyl-, thio-, and similarly modified forms of adenine, cytidine, guanine, thymine, and uridine which are not as easily recognized by endogenous endonucleases.

20 Many methods for introducing vectors into cells or tissues are available and equally suitable for use in vivo, in vitro, and ex vivo. For ex vivo therapy, vectors may be introduced into stem cells taken from the patient and clonally propagated for autologous transplant back into that same patient. Delivery by transfection, by liposome injections, or by polycationic amino polymers may be achieved using methods which are well known in the art. (See, e.g., Goldman, C.K. et al. (1997) Nat.
25 Biotechnol. 15:462-466.)

Any of the therapeutic methods described above may be applied to any subject in need of such therapy, including, for example, mammals such as humans, dogs, cats, cows, horses, rabbits, and monkeys.

An additional embodiment of the invention relates to the administration of a pharmaceutical
30 or sterile composition, in conjunction with a pharmaceutically acceptable carrier, for any of the therapeutic effects discussed above. Such pharmaceutical compositions may consist of NuABP, antibodies to NuABP, and mimetics, agonists, antagonists, or inhibitors of NuABP. The compositions may be administered alone or in combination with at least one other agent, such as a stabilizing compound, which may be administered in any sterile, biocompatible pharmaceutical carrier including,
35 but not limited to, saline, buffered saline, dextrose, and water. The compositions may be administered

to a patient alone, or in combination with other agents, drugs, or hormones.

The pharmaceutical compositions utilized in this invention may be administered by any number of routes including, but not limited to, oral, intravenous, intramuscular, intra-arterial, intramedullary, intrathecal, intraventricular, transdermal, subcutaneous, intraperitoneal, intranasal, enteral, topical, sublingual, or rectal means.

In addition to the active ingredients, these pharmaceutical compositions may contain suitable pharmaceutically-acceptable carriers comprising excipients and auxiliaries which facilitate processing of the active compounds into preparations which can be used pharmaceutically. Further details on techniques for formulation and administration may be found in the latest edition of Remington's

Pharmaceutical Sciences (Maack Publishing, Easton PA).

Pharmaceutical compositions for oral administration can be formulated using pharmaceutically acceptable carriers well known in the art in dosages suitable for oral administration. Such carriers enable the pharmaceutical compositions to be formulated as tablets, pills, dragees, capsules, liquids, gels, syrups, slurries, suspensions, and the like, for ingestion by the patient.

Pharmaceutical preparations for oral use can be obtained through combining active compounds with solid excipient and processing the resultant mixture of granules (optionally, after grinding) to obtain tablets or dragee cores. Suitable auxiliaries can be added, if desired. Suitable excipients include carbohydrate or protein fillers, such as sugars, including lactose, sucrose, mannitol, and sorbitol; starch from corn, wheat, rice, potato, or other plants; cellulose, such as methyl cellulose, hydroxypropylmethyl-cellulose, or sodium carboxymethylcellulose; gums, including arabic and tragacanth; and proteins, such as gelatin and collagen. If desired, disintegrating or solubilizing agents may be added, such as the cross-linked polyvinyl pyrrolidone, agar, and alginic acid or a salt thereof, such as sodium alginate.

Dragee cores may be used in conjunction with suitable coatings, such as concentrated sugar solutions, which may also contain gum arabic, talc, polyvinylpyrrolidone, carbopol gel, polyethylene glycol, and/or titanium dioxide, lacquer solutions, and suitable organic solvents or solvent mixtures. Dyestuffs or pigments may be added to the tablets or dragee coatings for product identification or to characterize the quantity of active compound, i.e., dosage.

Pharmaceutical preparations which can be used orally include push-fit capsules made of gelatin, as well as soft, sealed capsules made of gelatin and a coating, such as glycerol or sorbitol. Push-fit capsules can contain active ingredients mixed with fillers or binders, such as lactose or starches, lubricants, such as talc or magnesium stearate, and, optionally, stabilizers. In soft capsules, the active compounds may be dissolved or suspended in suitable liquids, such as fatty oils, liquid, or liquid polyethylene glycol with or without stabilizers.

Pharmaceutical formulations suitable for parenteral administration may be formulated in

aqueous solutions, preferably in physiologically compatible buffers such as Hanks' solution, Ringer's solution, or physiologically buffered saline. Aqueous injection suspensions may contain substances which increase the viscosity of the suspension, such as sodium carboxymethyl cellulose, sorbitol, or dextran. Additionally, suspensions of the active compounds may be prepared as appropriate oily injection suspensions. Suitable lipophilic solvents or vehicles include fatty oils, such as sesame oil, or synthetic fatty acid esters, such as ethyl oleate, triglycerides, or liposomes. Non-lipid polycationic amino polymers may also be used for delivery. Optionally, the suspension may also contain suitable stabilizers or agents to increase the solubility of the compounds and allow for the preparation of highly concentrated solutions.

For topical or nasal administration, penetrants appropriate to the particular barrier to be permeated are used in the formulation. Such penetrants are generally known in the art.

The pharmaceutical compositions of the present invention may be manufactured in a manner that is known in the art, e.g., by means of conventional mixing, dissolving, granulating, dragee-making, levigating, emulsifying, encapsulating, entrapping, or lyophilizing processes.

The pharmaceutical composition may be provided as a salt and can be formed with many acids, including but not limited to, hydrochloric, sulfuric, acetic, lactic, tartaric, malic, and succinic acids. Salts tend to be more soluble in aqueous or other protonic solvents than are the corresponding free base forms. In other cases, the preparation may be a lyophilized powder which may contain any or all of the following: 1 mM to 50 mM histidine, 0.1% to 2% sucrose, and 2% to 7% mannitol, at a pH range of 4.5 to 5.5, that is combined with buffer prior to use.

After pharmaceutical compositions have been prepared, they can be placed in an appropriate container and labeled for treatment of an indicated condition. For administration of NuABP, such labeling would include amount, frequency, and method of administration.

Pharmaceutical compositions suitable for use in the invention include compositions wherein the active ingredients are contained in an effective amount to achieve the intended purpose. The determination of an effective dose is well within the capability of those skilled in the art.

For any compound, the therapeutically effective dose can be estimated initially either in cell culture assays, e.g., of neoplastic cells, or in animal models such as mice, rats, rabbits, dogs, or pigs. An animal model may also be used to determine the appropriate concentration range and route of administration. Such information can then be used to determine useful doses and routes for administration in humans.

A therapeutically effective dose refers to that amount of active ingredient, for example NuABP or fragments thereof, antibodies of NuABP, and agonists, antagonists or inhibitors of NuABP, which ameliorates the symptoms or condition. Therapeutic efficacy and toxicity may be determined by standard pharmaceutical procedures in cell cultures or with experimental animals, such

WO 00/44900

PCT/US00/02237

as by calculating the ED_{50} (the dose therapeutically effective in 50% of the population) or LD_{50} (the dose lethal to 50% of the population) statistics. The dose ratio of toxic to therapeutic effects is the therapeutic index, which can be expressed as the LD_{50}/ED_{50} ratio. Pharmaceutical compositions which exhibit large therapeutic indices are preferred. The data obtained from cell culture assays and animal studies are used to formulate a range of dosage for human use. The dosage contained in such compositions is preferably within a range of circulating concentrations that includes the ED_{50} with little or no toxicity. The dosage varies within this range depending upon the dosage form employed, the sensitivity of the patient, and the route of administration.

The exact dosage will be determined by the practitioner, in light of factors related to the subject requiring treatment. Dosage and administration are adjusted to provide sufficient levels of the active moiety or to maintain the desired effect. Factors which may be taken into account include the severity of the disease state, the general health of the subject, the age, weight, and gender of the subject, time and frequency of administration, drug combination(s), reaction sensitivities, and response to therapy. Long-acting pharmaceutical compositions may be administered every 3 to 4 days, every week, or biweekly depending on the half-life and clearance rate of the particular formulation.

Normal dosage amounts may vary from about 0.1 μ g to 100,000 μ g, up to a total dose of about 1 gram, depending upon the route of administration. Guidance as to particular dosages and methods of delivery is provided in the literature and generally available to practitioners in the art.

Those skilled in the art will employ different formulations for nucleotides than for proteins or their inhibitors. Similarly, delivery of polynucleotides or polypeptides will be specific to particular cells, conditions, locations, etc.

DIAGNOSTICS

In another embodiment, antibodies which specifically bind NuABP may be used for the diagnosis of disorders characterized by expression of NuABP, or in assays to monitor patients being treated with NuABP or agonists, antagonists, or inhibitors of NuABP. Antibodies useful for diagnostic purposes may be prepared in the same manner as described above for therapeutics. Diagnostic assays for NuABP include methods which utilize the antibody and a label to detect NuABP in human body fluids or in extracts of cells or tissues. The antibodies may be used with or without modification, and may be labeled by covalent or non-covalent attachment of a reporter molecule. A wide variety of reporter molecules, several of which are described above, are known in the art and may be used.

A variety of protocols for measuring NuABP, including ELISAs, RIAs, and FACS, are known in the art and provide a basis for diagnosing altered or abnormal levels of NuABP expression.

Normal or standard values for NuABP expression are established by combining body fluids or cell

extracts taken from normal mammalian subjects, for example, human subjects, with antibody to NuABP under conditions suitable for complex formation. The amount of standard complex formation may be quantitated by various methods, such as photometric means. Quantities of NuABP expressed in subject, control, and disease samples from biopsied tissues are compared with the standard values.

5 Deviation between standard and subject values establishes the parameters for diagnosing disease.

In another embodiment of the invention, the polynucleotides encoding NuABP may be used for diagnostic purposes. The polynucleotides which may be used include oligonucleotide sequences, complementary RNA and DNA molecules, and PNAs. The polynucleotides may be used to detect and quantify gene expression in biopsied tissues in which expression of NuABP may be correlated
10 with disease. The diagnostic assay may be used to determine absence, presence, and excess expression of NuABP, and to monitor regulation of NuABP levels during therapeutic intervention.

In one aspect, hybridization with PCR probes which are capable of detecting polynucleotide sequences, including genomic sequences, encoding NuABP or closely related molecules may be used to identify nucleic acid sequences which encode NuABP. The specificity of the probe, whether it is
15 made from a highly specific region, e.g., the 5' regulatory region, or from a less specific region, e.g., a conserved motif, and the stringency of the hybridization or amplification will determine whether the probe identifies only naturally occurring sequences encoding NuABP, allelic variants, or related sequences.

Probes may also be used for the detection of related sequences, and may have at least 50%
20 sequence identity to any of the NuABP encoding sequences. The hybridization probes of the subject invention may be DNA or RNA and may be derived from the sequence of SEQ ID NO:56-110 or from genomic sequences including promoters, enhancers, and introns of the NuABP gene.

Means for producing specific hybridization probes for DNAs encoding NuABP include the cloning of polynucleotide sequences encoding NuABP or NuABP derivatives into vectors for the
25 production of mRNA probes. Such vectors are known in the art, are commercially available, and may be used to synthesize RNA probes in vitro by means of the addition of the appropriate RNA polymerases and the appropriate labeled nucleotides. Hybridization probes may be labeled by a variety of reporter groups, for example, by radionuclides such as ³²P or ³⁵S, or by enzymatic labels, such as alkaline phosphatase coupled to the probe via avidin/biotin coupling systems, and the like.

30 Polynucleotide sequences encoding NuABP may be used for the diagnosis of disorders associated with expression of NuABP. Examples of such disorders include, but are not limited to, a reproductive disorder such as disorders of prolactin production, infertility, including tubal disease, ovulatory defects, and endometriosis, disruptions of the estrous cycle, disruptions of the menstrual cycle, polycystic ovary syndrome, ovarian hyperstimulation syndrome, endometrial and ovarian
35 tumors, uterine fibroids, autoimmune disorders, ectopic pregnancies, and teratogenesis; cancer of the

breast, fibrocystic breast disease, and galactorrhea; disruptions of spermatogenesis, abnormal sperm physiology, cancer of the testis, cancer of the prostate, benign prostatic hyperplasia, prostatitis, Peyronie's disease, impotence, carcinoma of the male breast, and gynecomastia; an immune disorder such as inflammation, actinic keratosis, acquired immunodeficiency syndrome (AIDS), Addison's disease, adult respiratory distress syndrome, allergies, ankylosing spondylitis, amyloidosis, anemia, 5 arteriosclerosis, asthma, atherosclerosis, autoimmune hemolytic anemia, autoimmune thyroiditis, bronchitis, bursitis, cholecystitis, cirrhosis, contact dermatitis, Crohn's disease, atopic dermatitis, dermatomyositis, diabetes mellitus, emphysema, erythroblastosis fetalis, erythema nodosum, atrophic gastritis, glomerulonephritis, Goodpasture's syndrome, gout, Graves' disease, Hashimoto's thyroiditis, paroxysmal nocturnal hemoglobinuria, hepatitis, hypereosinophilia, irritable bowel syndrome, episodic lymphopenia with lymphocytotoxins, mixed connective tissue disease (MCTD), multiple sclerosis, myasthenia gravis, myocardial or pericardial inflammation, myelofibrosis, osteoarthritis, osteoporosis, pancreatitis, polycythemia vera, polymyositis, psoriasis, Reiter's syndrome, rheumatoid arthritis, scleroderma, Sjögren's syndrome, systemic anaphylaxis, systemic 15 lupus erythematosus, systemic sclerosis, primary thrombocythemia, thrombocytopenic purpura, ulcerative colitis, uveitis, Werner syndrome, complications of cancer, hemodialysis, and extracorporeal circulation, trauma, and hematopoietic cancer including lymphoma, leukemia, and myeloma; a neurological disorder such as epilepsy, ischemic cerebrovascular disease, stroke, cerebral neoplasms, Alzheimer's disease, Pick's disease, Huntington's disease, dementia, Parkinson's disease 20 and other extrapyramidal disorders, amyotrophic lateral sclerosis and other motor neuron disorders, progressive neural muscular atrophy, retinitis pigmentosa, hereditary ataxias, multiple sclerosis and other demyelinating diseases, bacterial and viral meningitis, brain abscess, subdural empyema, epidural abscess, suppurative intracranial thrombophlebitis, myelitis and radiculitis, viral central nervous system disease, prion diseases including kuru, Creutzfeldt-Jakob disease, and Gerstmann- 25 Straussler-Scheinker syndrome, fatal familial insomnia, nutritional and metabolic diseases of the nervous system, neurofibromatosis, tuberous sclerosis, cerebelloretinal hemangioblastomatosis, encephalotrigeminal syndrome, mental retardation and other developmental disorders of the central nervous system, cerebral palsy, neuroskeletal disorders, autonomic nervous system disorders, cranial nerve disorders, spinal cord diseases, muscular dystrophy and other neuromuscular disorders, 30 peripheral nervous system disorders, dermatomyositis and polymyositis, inherited, metabolic, endocrine, and toxic myopathies, myasthenia gravis, periodic paralysis, mental disorders including mood, anxiety, and schizophrenic disorders, akathisia, amnesia, catatonia, diabetic neuropathy, tardive dyskinesia, dystonias, paranoid psychoses, postherpetic neuralgia, and Tourette's disorder; and a cell proliferative disorder such as actinic keratosis, arteriosclerosis, atherosclerosis, bursitis, 35 cirrhosis, hepatitis, mixed connective tissue disease (MCTD), myelofibrosis, paroxysmal nocturnal

hemoglobinuria, polycythemia vera, psoriasis, primary thrombocythemia, and cancers including adenocarcinoma, leukemia, lymphoma, melanoma, myeloma, sarcoma, teratocarcinoma, and, in particular, cancers of the adrenal gland, bladder, bone, bone marrow, brain, breast, cervix, gall bladder, ganglia, gastrointestinal tract, heart, kidney, liver, lung, muscle, ovary, pancreas, parathyroid, 5 penis, prostate, salivary glands, skin, spleen, testis, thymus, thyroid, and uterus. The polynucleotide sequences encoding NuABP may be used in Southern or northern analysis, dot blot, or other membrane-based technologies; in PCR technologies; in dipstick, pin, and multiformat ELISA-like assays; and in microarrays utilizing fluids or tissues from patients to detect altered NuABP expression. Such qualitative or quantitative methods are well known in the art.

10 In a particular aspect, the nucleotide sequences encoding NuABP may be useful in assays that detect the presence of associated disorders, particularly those mentioned above. The nucleotide sequences encoding NuABP may be labeled by standard methods and added to a fluid or tissue sample from a patient under conditions suitable for the formation of hybridization complexes. After a suitable incubation period, the sample is washed and the signal is quantified and compared with a 15 standard value. If the amount of signal in the patient sample is significantly altered in comparison to a control sample then the presence of altered levels of nucleotide sequences encoding NuABP in the sample indicates the presence of the associated disorder. Such assays may also be used to evaluate the efficacy of a particular therapeutic treatment regimen in animal studies, in clinical trials, or to monitor the treatment of an individual patient.

20 In order to provide a basis for the diagnosis of a disorder associated with expression of NuABP, a normal or standard profile for expression is established. This may be accomplished by combining body fluids or cell extracts taken from normal subjects, either animal or human, with a sequence, or a fragment thereof, encoding NuABP, under conditions suitable for hybridization or amplification. Standard hybridization may be quantified by comparing the values obtained from 25 normal subjects with values from an experiment in which a known amount of a substantially purified polynucleotide is used. Standard values obtained in this manner may be compared with values obtained from samples from patients who are symptomatic for a disorder. Deviation from standard values is used to establish the presence of a disorder.

Once the presence of a disorder is established and a treatment protocol is initiated, 30 hybridization assays may be repeated on a regular basis to determine if the level of expression in the patient begins to approximate that which is observed in the normal subject. The results obtained from successive assays may be used to show the efficacy of treatment over a period ranging from several days to months.

With respect to cancer, the presence of an abnormal amount of transcript (either under- or 35 overexpressed) in biopsied tissue from an individual may indicate a predisposition for the

development of the disease, or may provide a means for detecting the disease prior to the appearance of actual clinical symptoms. A more definitive diagnosis of this type may allow health professionals to employ preventative measures or aggressive treatment earlier thereby preventing the development or further progression of the cancer.

5 Additional diagnostic uses for oligonucleotides designed from the sequences encoding NuABP may involve the use of PCR. These oligomers may be chemically synthesized, generated enzymatically, or produced in vitro. Oligomers will preferably contain a fragment of a polynucleotide encoding NuABP, or a fragment of a polynucleotide complementary to the polynucleotide encoding NuABP, and will be employed under optimized conditions for identification of a specific gene or
10 condition. Oligomers may also be employed under less stringent conditions for detection or quantification of closely related DNA or RNA sequences.

Methods which may also be used to quantify the expression of NuABP include radiolabeling or biotinylating nucleotides, coamplification of a control nucleic acid, and interpolating results from standard curves. (See, e.g., Melby, P.C. et al. (1993) *J. Immunol. Methods* 159:235-244; Duplaa, C.
15 et al. (1993) *Anal. Biochem.* 212:229-236.) The speed of quantitation of multiple samples may be accelerated by running the assay in a high-throughput format where the oligomer of interest is presented in various dilutions and a spectrophotometric or colorimetric response gives rapid quantitation.

In further embodiments, oligonucleotides or longer fragments derived from any of the
20 polynucleotide sequences described herein may be used as targets in a microarray. The microarray can be used to monitor the expression level of large numbers of genes simultaneously and to identify genetic variants, mutations, and polymorphisms. This information may be used to determine gene function, to understand the genetic basis of a disorder, to diagnose a disorder, and to develop and monitor the activities of therapeutic agents.

25 Microarrays may be prepared, used, and analyzed using methods known in the art. (See, e.g., Brennan, T.M. et al. (1995) U.S. Patent No. 5,474,796; Schena, M. et al. (1996) *Proc. Natl. Acad. Sci. USA* 93:10614-10619; Baldeschweiler et al. (1995) PCT application WO95/251116; Shalon, D. et al. (1995) PCT application WO95/35505; Heller, R.A. et al. (1997) *Proc. Natl. Acad. Sci. USA* 94:2150-2155; and Heller, M.J. et al. (1997) U.S. Patent No. 5,605,662.)

30 In another embodiment of the invention, nucleic acid sequences encoding NuABP may be used to generate hybridization probes useful in mapping the naturally occurring genomic sequence. The sequences may be mapped to a particular chromosome, to a specific region of a chromosome, or to artificial chromosome constructions, e.g., human artificial chromosomes (HACs), yeast artificial chromosomes (YACs), bacterial artificial chromosomes (BACs), bacterial P1 constructions, or single
35 chromosome cDNA libraries. (See, e.g., Harrington, J.J. et al. (1997) *Nat. Genet.* 15:345-355; Price,

C.M. (1993) Blood Rev. 7:127-134; and Trask, B.J. (1991) Trends Genet. 7:149-154.)

Fluorescent in situ hybridization (FISH) may be correlated with other physical chromosome mapping techniques and genetic map data. (See, e.g., Heinz-Ulrich, et al. (1995) in Meyers, supra, pp. 965-968.) Examples of genetic map data can be found in various scientific journals or at the
 5 Online Mendelian Inheritance in Man (OMIM) World Wide Web site. Correlation between the location of the gene encoding NuABP on a physical chromosomal map and a specific disorder, or a predisposition to a specific disorder, may help define the region of DNA associated with that disorder. The nucleotide sequences of the invention may be used to detect differences in gene sequences among normal, carrier, and affected individuals.

10 In situ hybridization of chromosomal preparations and physical mapping techniques, such as linkage analysis using established chromosomal markers, may be used for extending genetic maps. Often the placement of a gene on the chromosome of another mammalian species, such as mouse, may reveal associated markers even if the number or arm of a particular human chromosome is not known. New sequences can be assigned to chromosomal arms by physical mapping. This provides
 15 valuable information to investigators searching for disease genes using positional cloning or other gene discovery techniques. Once the disease or syndrome has been crudely localized by genetic linkage to a particular genomic region, e.g., ataxia-telangiectasia to 11q22-23, any sequences mapping to that area may represent associated or regulatory genes for further investigation. (See, e.g., Gatti, R.A. et al. (1988) Nature 336:577-580.) The nucleotide sequence of the subject invention may also be
 20 used to detect differences in the chromosomal location due to translocation, inversion, etc., among normal, carrier, or affected individuals.

In another embodiment of the invention, NuABP, its catalytic or immunogenic fragments, or oligopeptides thereof can be used for screening libraries of compounds in any of a variety of drug screening techniques. The fragment employed in such screening may be free in solution, affixed to a
 25 solid support, borne on a cell surface, or located intracellularly. The formation of binding complexes between NuABP and the agent being tested may be measured.

Another technique for drug screening provides for high throughput screening of compounds having suitable binding affinity to the protein of interest. (See, e.g., Geysen, et al. (1984) PCT application WO84/03564.) In this method, large numbers of different small test compounds are
 30 synthesized on a solid substrate. The test compounds are reacted with NuABP, or fragments thereof, and washed. Bound NuABP is then detected by methods well known in the art. Purified NuABP can also be coated directly onto plates for use in the aforementioned drug screening techniques. Alternatively, non-neutralizing antibodies can be used to capture the peptide and immobilize it on a solid support.

35 In another embodiment, one may use competitive drug screening assays in which neutralizing

antibodies capable of binding NuABP specifically compete with a test compound for binding NuABP. In this manner, antibodies can be used to detect the presence of any peptide which shares one or more antigenic determinants with NuABP.

In additional embodiments, the nucleotide sequences which encode NuABP may be used in any molecular biology techniques that have yet to be developed, provided the new techniques rely on properties of nucleotide sequences that are currently known, including, but not limited to, such properties as the triplet genetic code and specific base pair interactions.

Without further elaboration, it is believed that one skilled in the art can, using the preceding description, utilize the present invention to its fullest extent. The following embodiments are, therefore, to be construed as merely illustrative, and not limitative of the remainder of the disclosure in any way whatsoever.

Without further elaboration, it is believed that one skilled in the art can, using the preceding description, utilize the present invention to its fullest extent. The following preferred specific embodiments are, therefore, to be construed as merely illustrative, and not limitative of the remainder of the disclosure in any way whatsoever.

The disclosures of all patents, applications, and publications mentioned above and below, in particular U.S. Ser. No. 60/117,905 and U.S. Ser. No. 60/117,904, are hereby expressly incorporated by reference.

20

EXAMPLES

I. Construction of cDNA Libraries

RNA was purchased from Clontech or isolated from tissues described in Table 4. Some tissues were homogenized and lysed in guanidinium isothiocyanate, while others were homogenized and lysed in phenol or in a suitable mixture of denaturants, such as TRIZOL (Life Technologies), a monophasic solution of phenol and guanidine isothiocyanate. The resulting lysates were centrifuged over CsCl cushions or extracted with chloroform. RNA was precipitated from the lysates with either isopropanol or sodium acetate and ethanol, or by other routine methods.

Phenol extraction and precipitation of RNA were repeated as necessary to increase RNA purity. In some cases, RNA was treated with DNase. For most libraries, poly(A⁺) RNA was isolated using oligo d(T)-coupled paramagnetic particles (Promega), OLIGOTEX latex particles (QIAGEN, Chatsworth CA), or an OLIGOTEX mRNA purification kit (QIAGEN). Alternatively, RNA was isolated directly from tissue lysates using other RNA isolation kits, e.g., the POLY(A)PURE mRNA purification kit (Ambion, Austin TX).

In some cases, Stratagene was provided with RNA and constructed the corresponding cDNA libraries. Otherwise, cDNA was synthesized and cDNA libraries were constructed with the UNIZAP

vector system (Stratagene) or SUPERScript plasmid system (Life Technologies), using the recommended procedures or similar methods known in the art. (See, e.g., Ausubel, 1997, supra, units 5.1-6.6.) Reverse transcription was initiated using oligo d(T) or random primers. Synthetic oligonucleotide adapters were ligated to double stranded cDNA, and the cDNA was digested with the appropriate restriction enzyme or enzymes. For most libraries, the cDNA was size-selected (300-1000 bp) using SEPHACRYL S1000, SEPHAROSE CL2B, or SEPHAROSE CL4B column chromatography (Amersham Pharmacia Biotech) or preparative agarose gel electrophoresis. cDNAs were ligated into compatible restriction enzyme sites of the polylinker of a suitable plasmid, e.g., PBLUEScript plasmid (Stratagene), PSORT1 plasmid (Life Technologies), or pINCY (Incyte Pharmaceuticals, Palo Alto CA). Recombinant plasmids were transformed into competent *E. coli* cells including XL1-Blue, XL1-BlueMRF, or SOLR from Stratagene or DH5 α , DH10B, or ElectroMAX DH10B from Life Technologies.

II. Isolation of cDNA Clones

Plasmids were recovered from host cells by in vivo excision using the UNIZAP vector system (Stratagene) or by cell lysis. Plasmids were purified using at least one of the following: a Magic or WIZARD Minipreps DNA purification system (Promega); an AGTC Miniprep purification kit (Edge Biosystems, Gaithersburg MD); and QIAWELL 8 Plasmid, QIAWELL 8 Plus Plasmid, QIAWELL 8 Ultra Plasmid purification systems or the R.E.A.L. PREP 96 plasmid purification kit from QIAGEN. Following precipitation, plasmids were resuspended in 0.1 ml of distilled water and stored, with or without lyophilization, at 4°C.

Alternatively, plasmid DNA was amplified from host cell lysates using direct link PCR in a high-throughput format (Rao, V.B. (1994) Anal. Biochem. 216:1-14). Host cell lysis and thermal cycling steps were carried out in a single reaction mixture. Samples were processed and stored in 384-well plates, and the concentration of amplified plasmid DNA was quantified fluorometrically using PICOGREEN dye (Molecular Probes, Eugene OR) and a FLUOROSKAN II fluorescence scanner (Labsystems Oy, Helsinki, Finland).

III. Sequencing and Analysis

cDNA sequencing reactions were processed using standard methods or high-throughput instrumentation such as the ABI CATALYST 800 (Perkin-Elmer) thermal cycler or the PTC-200 thermal cycler (MJ Research) in conjunction with the HYDRA microdispenser (Robbins Scientific) or the MICROLAB 2200 (Hamilton) liquid transfer system. cDNA sequencing reactions were prepared using reagents provided by Amersham Pharmacia Biotech or supplied in ABI sequencing kits such as the ABI PRISM BIGDYE Terminator cycle sequencing ready reaction kit (Perkin-Elmer).

Electrophoretic separation of cDNA sequencing reactions and detection of labeled polynucleotides were carried out using the MEGABACE 1000 DNA sequencing system (Molecular Dynamics); the

ABI PRISM 373 or 377 sequencing system (Perkin-Elmer) in conjunction with standard ABI protocols and base calling software; or other sequence analysis systems known in the art. Reading frames within the cDNA sequences were identified using standard methods (reviewed in Ausubel, 1997, supra, unit 7.7). Some of the cDNA sequences were selected for extension using the techniques disclosed in Example V.

The polynucleotide sequences derived from cDNA sequencing were assembled and analyzed using a combination of software programs which utilize algorithms well known to those skilled in the art. Table 5 summarizes the tools, programs, and algorithms used and provides applicable descriptions, references, and threshold parameters. The first column of Table 5 shows the tools, programs, and algorithms used, the second column provides brief descriptions thereof, the third column presents appropriate references, all of which are incorporated by reference herein in their entirety, and the fourth column presents, where applicable, the scores, probability values, and other parameters used to evaluate the strength of a match between two sequences (the higher the score, the greater the homology between two sequences). Sequences were analyzed using MACDNASIS PRO software (Hitachi Software Engineering, South San Francisco CA) and LASERGENE software (DNASTAR). Polynucleotide and polypeptide sequence alignments were generated using the default parameters specified by the clustal algorithm as incorporated into the MEGALIGN multisequence alignment program (DNASTAR), which also calculates the percent identity between aligned sequences.

The polynucleotide sequences were validated by removing vector, linker, and polyA sequences and by masking ambiguous bases, using algorithms and programs based on BLAST, dynamic programming, and dinucleotide nearest neighbor analysis. The sequences were then queried against a selection of public databases such as the GenBank primate, rodent, mammalian, vertebrate, and eukaryote databases, and BLOCKS, PRINTS, DOMO, PRODOM, and PFAM to acquire annotation using programs based on BLAST, FASTA, and BLIMPS. The sequences were assembled into full length polynucleotide sequences using programs based on Phred, Phrap, and Consed, and were screened for open reading frames using programs based on GeneMark, BLAST, and FASTA. The full length polynucleotide sequences were translated to derive the corresponding full length amino acid sequences, and these full length sequences were subsequently analyzed by querying against databases such as the GenBank databases (described above), SwissProt, BLOCKS, PRINTS, DOMO, PRODOM, Prosite, and Hidden Markov Model (HMM)-based protein family databases such as PFAM. HMM is a probabilistic approach which analyzes consensus primary structures of gene families. (See, e.g., Eddy, S.R. (1996) *Curr. Opin. Struct. Biol.* 6:361-365.)

The programs described above for the assembly and analysis of full length polynucleotide and amino acid sequences were also used to identify polynucleotide sequence fragments from SEQ ID

NO:56-110. Fragments from about 20 to about 4000 nucleotides which are useful in hybridization and amplification technologies were described in The Invention section above.

IV. Northern Analysis

Northern analysis is a laboratory technique used to detect the presence of a transcript of a gene and involves the hybridization of a labeled nucleotide sequence to a membrane on which RNAs from a particular cell type or tissue have been bound. (See, e.g., Sambrook, supra, ch. 7; Ausubel, 1995, supra, ch. 4 and 16.)

Analogous computer techniques applying BLAST were used to search for identical or related molecules in nucleotide databases such as GenBank or LIFESEQ (Incyte Pharmaceuticals). This analysis is much faster than multiple membrane-based hybridizations. In addition, the sensitivity of the computer search can be modified to determine whether any particular match is categorized as exact or similar. The basis of the search is the product score, which is defined as:

$$\frac{\% \text{ sequence identity} \times \% \text{ maximum BLAST score}}{100}$$

The product score takes into account both the degree of similarity between two sequences and the length of the sequence match. For example, with a product score of 40, the match will be exact within a 1% to 2% error, and, with a product score of 70, the match will be exact. Similar molecules are usually identified by selecting those which show product scores between 15 and 40, although lower scores may identify related molecules.

The results of northern analyses are reported as a percentage distribution of libraries in which the transcript encoding NuABP occurred. Analysis involved the categorization of cDNA libraries by organ/tissue and disease. The organ/tissue categories included cardiovascular, dermatologic, developmental, endocrine, gastrointestinal, hematopoietic/immune, musculoskeletal, nervous, reproductive, and urologic. The disease/condition categories included cancer, inflammation, trauma, cell proliferation, neurological, and pooled. For each category, the number of libraries expressing the sequence of interest was counted and divided by the total number of libraries across all categories. Percentage values of tissue-specific and disease- or condition-specific expression are reported in Table 3.

V. Extension of NuABP Encoding Polynucleotides

The full length nucleic acid sequences of SEQ ID NO:56-110 were produced by extension of an appropriate fragment of the full length molecule using oligonucleotide primers designed from this fragment. One primer was synthesized to initiate 5' extension of the known fragment, and the other primer, to initiate 3' extension of the known fragment. The initial primers were designed using OLIGO 4.06 software (National Biosciences), or another appropriate program, to be about 22 to 30 nucleotides in length, to have a GC content of about 50% or more, and to anneal to the target

Step 5: steps 2, 3, and 4 repeated 29 times; Step 6: 72°C, 5 min; Step 7: storage at 4°C. DNA was quantified by PICOGREEN reagent (Molecular Probes) as described above. Samples with low DNA recoveries were reamplified using the same conditions as described above. Samples were diluted with 20% dimethylsulfoxide (1:2, v/v), and sequenced using DYENAMIC energy transfer sequencing primers and the DYENAMIC DIRECT kit (Amersham Pharmacia Biotech) or the ABI PRISM BIGDYE Terminator cycle sequencing ready reaction kit (Perkin-Elmer).

In like manner, the nucleotide sequences of SEQ ID NO:56-110 are used to obtain 5' regulatory sequences using the procedure above, oligonucleotides designed for such extension, and an appropriate genomic library.

10 VI. Labeling and Use of Individual Hybridization Probes

Hybridization probes derived from SEQ ID NO:56-110 are employed to screen cDNAs, genomic DNAs, or mRNAs. Although the labeling of oligonucleotides, consisting of about 20 base pairs, is specifically described, essentially the same procedure is used with larger nucleotide fragments. Oligonucleotides are designed using state-of-the-art software such as OLIGO 4.06 software (National Biosciences) and labeled by combining 50 pmol of each oligomer, 250 μ Ci of [γ -³²P] adenosine triphosphate (Amersham Pharmacia Biotech), and T4 polynucleotide kinase (DuPont NEN, Boston MA). The labeled oligonucleotides are substantially purified using a SEPHADEX G-25 superfine size exclusion dextran bead column (Amersham Pharmacia Biotech). An aliquot containing 10⁷ counts per minute of the labeled probe is used in a typical membrane-based hybridization analysis of human genomic DNA digested with one of the following endonucleases: 20 Ase I, Bgl II, Eco RI, Pst I, Xba I, or Pvu II (DuPont NEN).

The DNA from each digest is fractionated on a 0.7% agarose gel and transferred to nylon membranes (Nytran Plus, Schleicher & Schuell, Durham NH). Hybridization is carried out for 16 hours at 40°C. To remove nonspecific signals, blots are sequentially washed at room temperature under conditions of up to, for example, 0.1 x saline sodium citrate and 0.5% sodium dodecyl sulfate. Hybridization patterns are visualized using autoradiography or an alternative imaging means and compared.

VII. Microarrays

A chemical coupling procedure and an ink jet device can be used to synthesize array elements on the surface of a substrate. (See, e.g., Baldeschweiler, supra.) An array analogous to a dot or slot blot may also be used to arrange and link elements to the surface of a substrate using thermal, UV, chemical, or mechanical bonding procedures. A typical array may be produced by hand or using available methods and machines and contain any appropriate number of elements. After hybridization, nonhybridized probes are removed and a scanner used to determine the levels and patterns of fluorescence. The degree of complementarity and the relative abundance of each probe 35

which hybridizes to an element on the microarray may be assessed through analysis of the scanned images.

Full-length cDNAs, Expressed Sequence Tags (ESTs), or fragments thereof may comprise the elements of the microarray. Fragments suitable for hybridization can be selected using software well known in the art such as LASERGENE software (DNASTAR). Full-length cDNAs, ESTs, or fragments thereof corresponding to one of the nucleotide sequences of the present invention, or selected at random from a cDNA library relevant to the present invention, are arranged on an appropriate substrate, e.g., a glass slide. The cDNA is fixed to the slide using, e.g., UV cross-linking followed by thermal and chemical treatments and subsequent drying. (See, e.g., Schena, M. et al. (1995) Science 270:467-470; Shalon, D. et al. (1996) Genome Res. 6:639-645.) Fluorescent probes are prepared and used for hybridization to the elements on the substrate. The substrate is analyzed by procedures described above.

VIII. Complementary Polynucleotides

Sequences complementary to the NuABP-encoding sequences, or any parts thereof, are used to detect, decrease, or inhibit expression of naturally occurring NuABP. Although use of oligonucleotides comprising from about 15 to 30 base pairs is described, essentially the same procedure is used with smaller or with larger sequence fragments. Appropriate oligonucleotides are designed using OLIGO 4.06 software (National Biosciences) and the coding sequence of NuABP. To inhibit transcription, a complementary oligonucleotide is designed from the most unique 5' sequence and used to prevent promoter binding to the coding sequence. To inhibit translation, a complementary oligonucleotide is designed to prevent ribosomal binding to the NuABP-encoding transcript.

IX. Expression of NuABP

Expression and purification of NuABP is achieved using bacterial or virus-based expression systems. For expression of NuABP in bacteria, cDNA is subcloned into an appropriate vector containing an antibiotic resistance gene and an inducible promoter that directs high levels of cDNA transcription. Examples of such promoters include, but are not limited to, the *trp-lac (tac)* hybrid promoter and the T5 or T7 bacteriophage promoter in conjunction with the *lac* operator regulatory element. Recombinant vectors are transformed into suitable bacterial hosts, e.g., BL21(DE3). Antibiotic resistant bacteria express NuABP upon induction with isopropyl beta-D-thiogalactopyranoside (IPTG). Expression of NuABP in eukaryotic cells is achieved by infecting insect or mammalian cell lines with recombinant Autographica californica nuclear polyhedrosis virus (AcMNPV), commonly known as baculovirus. The nonessential polyhedrin gene of baculovirus is replaced with cDNA encoding NuABP by either homologous recombination or bacterial-mediated transposition involving transfer plasmid intermediates. Viral infectivity is maintained and the strong polyhedrin promoter drives high levels of cDNA transcription. Recombinant baculovirus is used to

WO 00/44900

PCT/US00/02237

infect Spodoptera frugiperda (Sf9) insect cells in most cases, or human hepatocytes, in some cases. Infection of the latter requires additional genetic modifications to baculovirus. (See Engelhard, E.K. et al. (1994) Proc. Natl. Acad. Sci. USA 91:3224-3227; Sandig, V. et al. (1996) Hum. Gene Ther. 7:1937-1945.)

In most expression systems, NuABP is synthesized as a fusion protein with, e.g., glutathione S-transferase (GST) or a peptide epitope tag, such as FLAG or 6-His, permitting rapid, single-step, affinity-based purification of recombinant fusion protein from crude cell lysates. GST, a 26-kilodalton enzyme from Schistosoma japonicum, enables the purification of fusion proteins on immobilized glutathione under conditions that maintain protein activity and antigenicity (Amersham Pharmacia Biotech). Following purification, the GST moiety can be proteolytically cleaved from NuABP at specifically engineered sites. FLAG, an 8-amino acid peptide, enables immunoaffinity purification using commercially available monoclonal and polyclonal anti-FLAG antibodies (Eastman Kodak). 6-His, a stretch of six consecutive histidine residues, enables purification on metal-chelate resins (QIAGEN). Methods for protein expression and purification are discussed in Ausubel (1995, supra, ch. 10 and 16). Purified NuABP obtained by these methods can be used directly in the following activity assay.

X. Demonstration of NuABP Activity

NuABP activity is measured by its ability to stimulate transcription of a reporter gene (Liu, H.Y. et al. (1997) EMBO J. 16(17):5289-5298.) The assay entails the use of a well characterized reporter gene construct, LexA_{op}-LacZ, that consists of LexA DNA transcriptional control elements (LexA_{op}) fused to sequences encoding the E. coli LacZ enzyme. The methods for constructing and expressing fusions genes, introducing them into cells, and measuring LacZ enzyme activity, are well known to those skilled in the art. Sequences encoding NuABP are cloned into a plasmid that directs the synthesis of a fusion protein, LexA-NuABP, consisting of NuABP and a DNA binding domain derived from the LexA transcription factor. The resulting plasmid, encoding a LexA-NuABP fusion protein, is introduced into yeast cells along with a plasmid containing the LexA_{op}-LacZ reporter gene. The amount of LacZ enzyme activity associated with LexA-NuABP transfected cells, relative to control cells, is proportional to the amount of transcription stimulated by the NuABP.

XI. Functional Assays

NuABP function is assessed by expressing the sequences encoding NuABP at physiologically elevated levels in mammalian cell culture systems. cDNA is subcloned into a mammalian expression vector containing a strong promoter that drives high levels of cDNA expression. Vectors of choice include pCMV SPORT (Life Technologies) and pCR3.1 (Invitrogen, Carlsbad CA), both of which contain the cytomegalovirus promoter. 5-10 µg of recombinant vector are transiently transfected into a human cell line, for example, an endothelial or hematopoietic cell

line, using either liposome formulations or electroporation. 1-2 μ g of an additional plasmid containing sequences encoding a marker protein are co-transfected. Expression of a marker protein provides a means to distinguish transfected cells from nontransfected cells and is a reliable predictor of cDNA expression from the recombinant vector. Marker proteins of choice include, e.g., Green Fluorescent Protein (GFP; Clontech), CD64, or a CD64-GFP fusion protein. Flow cytometry (FCM), an automated, laser optics-based technique, is used to identify transfected cells expressing GFP or CD64-GFP and to evaluate the apoptotic state of the cells and other cellular properties. FCM detects and quantifies the uptake of fluorescent molecules that diagnose events preceding or coincident with cell death. These events include changes in nuclear DNA content as measured by staining of DNA with propidium iodide; changes in cell size and granularity as measured by forward light scatter and 90 degree side light scatter; down-regulation of DNA synthesis as measured by decrease in bromodeoxyuridine uptake; alterations in expression of cell surface and intracellular proteins as measured by reactivity with specific antibodies; and alterations in plasma membrane composition as measured by the binding of fluorescein-conjugated Annexin V protein to the cell surface. Methods in flow cytometry are discussed in Ormerod, M.G. (1994) *Flow Cytometry*, Oxford, New York NY.

The influence of NuABP on gene expression can be assessed using highly purified populations of cells transfected with sequences encoding NuABP and either CD64 or CD64-GFP. CD64 and CD64-GFP are expressed on the surface of transfected cells and bind to conserved regions of human immunoglobulin G (IgG). Transfected cells are efficiently separated from nontransfected cells using magnetic beads coated with either human IgG or antibody against CD64 (DYNAL, Lake Success NY). mRNA can be purified from the cells using methods well known by those of skill in the art. Expression of mRNA encoding NuABP and other genes of interest can be analyzed by northern analysis or microarray techniques.

XII. Production of NuABP Specific Antibodies

25 NuABP substantially purified using polyacrylamide gel electrophoresis (PAGE; see, e.g., Harrington, M.G. (1990) *Methods Enzymol.* 182:488-495), or other purification techniques, is used to immunize rabbits and to produce antibodies using standard protocols.

Alternatively, the NuABP amino acid sequence is analyzed using LASERGENE software (DNASTAR) to determine regions of high immunogenicity, and a corresponding oligopeptide is synthesized and used to raise antibodies by means known to those of skill in the art. Methods for selection of appropriate epitopes, such as those near the C-terminus or in hydrophilic regions are well described in the art. (See, e.g., Ausubel, 1995, *supra*, ch. 11.)

Typically, oligopeptides of about 15 residues in length are synthesized using an ABI 431A peptide synthesizer (Perkin-Elmer) using fmoc-chemistry and coupled to KLH (Sigma-Aldrich, St. Louis MO) by reaction with N-maleimidobenzoyl-N-hydroxysuccinimide ester (MBS) to increase

immunogenicity. (See, e.g., Ausubel, 1995, supra.) Rabbits are immunized with the oligopeptide-KLH complex in complete Freund's adjuvant. Resulting antisera are tested for antipeptide and anti-NuABP activity by, for example, binding the peptide or NuABP to a substrate, blocking with 1% BSA, reacting with rabbit antisera, washing, and reacting with radio-iodinated goat anti-rabbit IgG.

5 **XIII. Purification of Naturally Occurring NuABP Using Specific Antibodies**

Naturally occurring or recombinant NuABP is substantially purified by immunoaffinity chromatography using antibodies specific for NuABP. An immunoaffinity column is constructed by covalently coupling anti-NuABP antibody to an activated chromatographic resin, such as CNBr-activated SEPHAROSE (Amersham Pharmacia Biotech). After the coupling, the resin is
10 blocked and washed according to the manufacturer's instructions.

Media containing NuABP are passed over the immunoaffinity column, and the column is washed under conditions that allow the preferential absorbance of NuABP (e.g., high ionic strength buffers in the presence of detergent). The column is eluted under conditions that disrupt antibody/NuABP binding (e.g., a buffer of pH 2 to pH 3, or a high concentration of a chaotrope, such
15 as urea or thiocyanate ion), and NuABP is collected.

XIV. Identification of Molecules Which Interact with NuABP

NuABP, or biologically active fragments thereof, are labeled with ¹²⁵I Bolton-Hunter reagent. (See, e.g., Bolton A.E. and W.M. Hunter (1973) Biochem. J. 133:529-539.) Candidate molecules previously arrayed in the wells of a multi-well plate are incubated with the labeled NuABP, washed,
20 and any wells with labeled NuABP complex are assayed. Data obtained using different concentrations of NuABP are used to calculate values for the number, affinity, and association of NuABP with the candidate molecules.

Various modifications and variations of the described methods and systems of the invention will be apparent to those skilled in the art without departing from the scope and spirit of the invention.
25 Although the invention has been described in connection with certain embodiments, it should be understood that the invention as claimed should not be unduly limited to such specific embodiments. Indeed, various modifications of the described modes for carrying out the invention which are obvious to those skilled in molecular biology or related fields are intended to be within the scope of the following claims.

TABLE 1

Protein SEQ ID No:	Nucleotide SEQ ID NO:	Clone ID	Library	Fragments
1	56	025733	SPLNFET01	025733H1 and 025733X307D2 (SPLNFET01), 1519809F1 and 1519809T1 (BLADTUT04), 1526288T6 (UCMCL5T01), 1595557X16C1 and 1595557X19C1 (BRAINT014), 1903359F6 (OVARNOT07), 2417225F6 (HNT3AZT01), 4283542H1 (LIVRDIR01)
2	57	079702	SYNORAB01	002190H1 (U937NOT01), 079479F1 and 079702H1 (SYNORAB01), 125223T6 (LUNGNOT01), 371006R6 (LUNGNOT02), 2129460T6 (KIDNNOT05), 2999366H1 (TLYMNOT06), 3031905F6 (TLYMNOT05), 4949863H1 (SINTNOT25)
3	58	116208	KIDNNOT01	116208H1 and 116208R1 (KIDNNOT01), 2293058R6 (BRAINON01), 3731418H1 and 3731418T6 (SMCCNON03)
4	59	179261	PLACNOB01	179261H1 (PLACNOB01), 3666231F6 and 3666231T6 (PANCNOT16)
5	60	259161	HNT2RAT01	259161H1 (HNT2RAT01), 1005021R6 (BRSTNOT03), 2634660H1 (COLNTUT15), 2894335H1 (KIDNTUT14), 2924845H1 (SININOT04), 3659440H1 (ENDPNOT02), SBMA02955F1, SBMA03577F1, SBMA01445F1, SBMA00985F1, SBMA01499F1
6	61	320087	EOSIHET02	016657F1 (HUVLPB01), 320087H1 (EOSIHET02), 824110R1 (PROSNOT06), 987467H1 (LVENNOT03), 1235752F1 (LUNGFET03), 1361280F1 (LUNGNOT12), 1389740H1 (EOSINOT01), 1534332F1 (SPLNNOT04), 1813754F6 (SKINBIT01), 4184915H1 (BRSTNOT31), 5306522H1 (MONOTXT02)
7	62	491271	HNT2AGT01	363816X3 and 363816X9 (PROSNOT01), 491271F1, 491271H1 and 491271T6 (HNT2AGT01), 967354R6, 967354X15 and 967354X27 (BRSTNOT05), 2733444H1 (OVARTUT04)
8	63	585172	PROSNOT02	395188R6 (TMLR2DT01), 585172H1 (PROSNOT02), 864269T1 (BRAITUT03), 1417965F1 (KIDNNOT09)
9	64	615200	COLNTUT02	615200H1 and 615200R6 (COLNTUT02), 1213980R1 (BRSTTUT01), SBPA02731DL, SBPA00184D1
10	65	997067	KIDNTUT01	125981X3 (LJUNGNOT01), 997067H1, 997067R6 and 997067T6 (KIDNTUT01), 1448201H1 (PLACNOT02), 1663447H1 (BRSTNOT09), 1889314H1 (BLADTUT07), 1918706H1 (PROSNOT06), 2699956H1 (OVARTUT10), 2702585H1 (OVARTUT10), 2900479H1 (DRGCNOT01), 3595727T6 (FIBPNOT01), 4309131H1 (BRAUNOT01)
11	66	144326 2	THYRN03	1257005F1 (MENITUT03), 1443262H1 (THYRN03), 1618906F6 (BRAITUT12), 2474133T6 (THP1NOT03), 3594075H1 (FIBPNOT01), 4914442H1 (LIVRFET05)

TABLE 1 (cont.)

Protein SEQ ID No:	Nucleotide SEQ ID NO:	Clone ID	Library	Fragments
12	67	152164 8	BLADTUT04	292172H1 (TMLR3DT01), 819925R6 (KERANOT02), 1353913H1 (LATRTUT02), 1521648H1 and 1522364F1 (BLADTUT04), 1963178H1 (BRSTNOT04), 2342505F6 (TESTTUT02), 4899970H1 (OVARDT01), 5043585H2 (PLACFER01)
13	68	168549 4	PROSNOT15	903980X13, 903980X14 and 903980X17 (COLNNOT07), 1685494H1 (PROSNOT15), 4164127T6 (BRSTNOT32)
14	69	173082 9	BRSTTUT08	116146R1 (KIDNNOT01), 836856R1 (PROSNOT07), 1730829H1, 1730829X11C1, 1730829X12C1 and 1730829X13C1 (BRSTTUT08), 1959889R6 (BRSTNOT04), 2188079H1 (PROSNOT26), 3384625H1 (ESOGNOT04)
15	70	186464 1	PROSNOT19	1844972H1 (COLNNOT08), 1864641F6 and 1864641H1 (PROSNOT19), 3090702T6 (BRSTNOT19), 3411665H1 (BRSTTUS08), 5152366H1 (HEARFET03), 5166179H1 (MUSCDMT01)
16	71	244460 4	THP1NOT03	1506658F1 (BRAITUT07), 1532034F1 (SPLNNOT04), 2444604H1 (THP1NOT03)
17	72	244500 8	THP1NOT03	605598X12 (BRSTTUT01), 628644H1 (KIDNNOT05), 732124R1 (LUNGNOT03), 819194R1 (KERANOT02), 1259467H1 (MENITUT03), 1363205F6 (LUNGNOT12), 1901312T6 (BLADTUT06), 2445008H1 (THP1NOT03), 2681125H1 (SINIUCT01)
18	73	257246 2	HIPOAZT01	396323R6 (PITUNOT02), 863622H1 (BRAITUT03), 1848956F6 and 1848956T6 (LUNGFET03), 2345947H1 (TESTTUT02), 2396384F6 (THP1AZT01), 2572462H1 (HIPOAZT01), 2650980F6 (LUNGUT12), 2814325H1 (OVARNOT10), 5076051H1 (COLCTUT03)
19	74	257289 2	HIPOAZT01	030596X15R1 (THP1NOB01), 539564X11 (LNODNOT02), 1275514F1 and 1275514T6 (TESTTUT02), 2112383H1 (BRAITUT03), 2572892H1 (HIPOAZT01), 2986518H1 (CARGDIT01)
20	75	278567 4	BRSTNOT13	261399H1 (HNT2AGT01), 1274739F1 (TESTTUT02), 2785674H1 (BRSTNOT13)
21	76	279747 9	NPOLNOT01	302614X13 (TESTNOT04), 2797479H1 (NPOLNOT01), SAIA02597F1, SAIA00739F1, SAIA02537F1
22	77	296064 0	ADRENOT09	027211R1, 027211X1 and 027211X3 (SPLNFET01), 1401538F6 (BRAITUT08), 2496984F6 (ADRETUT05), 2960640H1 (ADRENOT09), 3211036T6 (BLADNOT08)
23	78	345405 1	SPLNNOT11	279331R6 (LIVRNOT02), 2515972T6 and 2516010T6 (LIVRTUT04), 2910726F6 (KIDNTUT15), 3454051H1 (SPLNNOT11)

TABLE 1 (cont.)

Protein SEQ ID NO:	Nucleotide SEQ ID NO:	Clone ID	Library	Fragments
24	79	351064 0	CONCNOT01	556354H1 (MPHGLPT02), 581085H1 (BRAVYXT05), 990636R6 (COLNNOT11), 1799185F6 and 1799185T6 (COLNNOT27), 3510640H1 (CONCNOT01), 4326648H1 (TLYMUNT01), SBHA01099F1
25	80	381508 3	TONSNOT03	2026951R6 and 2026951T6 (KERANOT02), 2300211R6 (BRSTNOT05), 2505283F6 (CONUTUT01), 3187267R6 (THYMNON04), 3815083H1 and 3815083T6 (TONSNOT03)
26	81	398845 7	LUNGNON03	609622R6 (COLNNOT01), 1710465F6 (PROSNOT16), 3988457H1 (LUNGNON03), SAQA00089F1, SAQA03055F1, SAQB00279F1
27	82	131890	BMARNOT02	131890H1 (BMARNOT02), 131890T6 (BMARNOT02), 132849R6 (BMARNOT02), 3357071F6 (PROSTUT16)
28	83	238642	SINTNOT02	238642H1 (SINTNOT02), 1620593F6 (BRAITUT13), 1620593H1 (BRAITUT13), 1620593T6 (BRAITUT13), 2534087F6 (BRAINOT18)
29	84	669862	CRBLNOT01	347231X7 (THYMNOT02), 669862H1 (CRBLNOT01), 2244458R6 (HIPONON02), 2244458T6 (HIPONON02), 2622610T6 (KERANOT02), 3536262H1 (KIDNNOT25), 4204212H1 (BRAITUT29)
30	85	100366 3	BRSTNOT03	850478T1 (NGANNOT01), 1003663H1 (BRSTNOT03), 1252179F2 (LUNGFET03), 1293333F1 (PGANNOT03), 1813002F6 (PROSTUT12), 2101974R6 (BRAITUT02)
31	86	143255 7	BEPINON01	1314545F6 (BLADTUT02), 1432557H1 (BEPINON01), 1443311R1 (THYRNOT03), 1705738F6 (DUODNOT02), 2182184F6 (SININOT01)
32	87	144177 0	THYRNOT03	035105R1 (HUVENOB01), 1441770H1 (THYRNOT03), 1500943F1 (SINTBST01), 2542840H1 (UTRSNOT11), 4533672H1 (OVARNOT12)
33	88	145668 4	COLNFET02	1456684F6 (COLNFET02), 1456684H1 (COLNFET02), 1456684T6 (COLNFET02), 1992143H1 (CORPNOT02), 2687476F6 (LUNGNOT23), 3139175F6 (SMCCNOT02), 4746319H1 (SMCRUNT01)
34	89	160291 6	BLADNOT03	3397976X305D2 (UTRSNOT16)
35	90	169281 6	COLNNOT23	999017R6 (KIDNUTUT01), 1342490T1 (COLNUTUT03), 1421981F1 (KIDNNOT09), 1692816H1 (COLNNOT23), 2176832F6 (ENDCNOT03), 2451404F6 (ENDANOT01)
36	91	196819 1	BRSTNOT04	1968191H1 (BRSTNOT04), 1968191T6 (BRSTNOT04), 2752967R6 (THPIAZS08), 3281163T6 (STOMFET02), 3748607H1 (UTRSNOT18)
37	92	205206 1	LIVRFET02	003803X8 (HMCINOT01), 027044X1 (SPLNFET01), 027044X101 (SPLNFET01), 2052061H1 (LIVRFET02), 3931936F6 (PROSTUT09)

TABLE 1 (cont.)

Protein SEQ ID NO:	Nucleotide SEQ ID NO:	Clone ID	Library	Fragments
38	93	205620 7	BEPINOT01	071525F1 (PLACNOB01), 162720R1 (ADENINB01), 270498H1 (HNT2NOT01), 1477853T1 (CORPNOT02), 1931058F6 (COLNTUT03), 2056207H1 (BEPINOT01), 2056207X1I1R1 (BEPINOT01), 2231060F6 (PROSNOT16), 2420063X309D4 (SCORNON02), 3424630H1 (BRSTNOR01), 3873760F6 (HEARNOT06), 3873760T6 (HEARNOT06), SBOA00627D1, SCJA02192V1, SCJA02089V1
39	94	210180 3	BRAITUT02	399584R6 (PITUNOT02), 399584T6 (PITUNOT02), 1649058F6 (PROSTUT09), 1902809F6 (OVARNOT07), 2101803H1 (BRAITUT02), 2101803R6 (BRAITUT02), 3098623H1 (CERVNOT03)
40	95	211236 2	BRAITUT03	948628R1 (PANCNOT05), 1209447T1 (BRSTNOT02), 1814624F6 (PROSNOT20), 2112362H1 (BRAITUT03), 2945621H1 (BRAITUT23), 3285663H1 (HEAONOT05), 3526403H1 (ESOGTUN01), 5032729H1 (ENDIUNT01), 5099417H1 (PROSTUS20)
41	96	211734 6	BRSTTUT02	487994R6 (HNT2AGT01), 952855R1 (SCORNON01), 952855T1 (SCORNON01), 2117346H1 (BRSTTUT02), 2458342F6 (ENDANOT01), 2731585H1 (OVARTUT04), 3475780H1 (LUNGNOT27), 3538525F6 (SEMVTOT04)
42	97	211991 7	BRSTTUT02	2119917H1 (BRSTTUT02), 2791421F6 (COLNTUT16), 2794083F6 (COLNTUT16), 5006921H1 (STOMNOT08)
43	98	212345 6	BRSTNOT07	484031H1 (HNT2RAT01), 617559F1 (PGANNOT01), 617559R1 (PGANNOT01), 1575977F1 (LNODNOT03), 2123456H1 (BRSTNOT07), 2958712H1 (ADRENOT09), 3764961H1 (BRSTNOT24)
44	99	214879 2	BRAINOT09	1732781F6 (BRSTTUT08), 2050885F6 (LIVRFET02), 2148792H1 (BRAINOT09), 2590822H1 (LUNGNOT22), 2972368T6 (HEAONOT02), SBQA00396D1, SEQA03678D1, SBQA02120D1, SBQA03269D1
45	100	275194 3	THP1AZS08	1720187X16C1 (BLADNOT06), 2751943H1 (THP1AZS08), 3492378H1 (ADRETUT07)
46	101	312891 3	LUNGUT12	2551859F6 (LUNGUT06), 3128913H1 (LUNGUT12), SBMA01861F1, SBMA02298F1, SBMA01013F1, SBMA02403F1, SBMA01362F1
47	102	328294 1	HEAONOT05	154741R6 (THP1PLB02), 155904R6 (THP1PLB02), 157816R1 (THP1PLB02), 979920H1 (TONGTUT01), 1233933T6 (LUNGFEF03), 1657077F6 (URETTUT01), 2445017F6 (THPINOT03), 3282941H1 (HEAONOT05), 3341633H1 (SPLNNOT09), 3517140H1 (LUNGNGN03)
48	103	328665 6	HEAONOT05	898123H1 (BRSTNOT05), 3286656H1 (HEAONOT05), 3641429T6 (LUNGNGN03), 3657668F6 (ENDPNOT02)

TABLE 1 (cont.)

Protein SEQ ID NO:	Nucleotide SEQ ID NO:	Clone ID	Library	Fragments
49	104	349080 2	EPIGNOT01	2238441H1 (PANCUTUT02), 2700133F6 (OVRTUT10), 2700133T6 (OVRTUT10), 3490226H1 (EPIGNOT01), 3490802H1 (EPIGNOT01), 4822929H1 (PROSTUT17)
50	105	350736 6	CONCNOT01	2130284H1 (KIDNNOT05), 3507366H1 (CONCNOT01), 3557087F6 (LUNGNOT31), 4241774H1 (SYNWDIT01)
51	105	357306 0	BRONNOT01	3573060F6 (BRONNOT01), 3573060H1 (BRONNOT01), 3573060T6 (BRONNOT01), 3867263H1 (BRAITUT07), 5013346H1 (BRAXNOT03)
52	107	357366 1	BRONNOT01	3028034F6 (HEARFET02), 3152642H1 (ADRENON04), 3573661F6 (BRONNOT01), 3573661H1 (BRONNOT01), 3577568F6 (BRONNOT01)
53	108	363342 2	LIVRNOT03	033412R6 (THP1NOB01), 074123F1 (THP1PEB01), 263241H1 (HNT2AGT01), 748567R1 (BRAITUT01), 1292088T1 (PGANNOT03), 1517449T1 (PANCUTUT01), 3633422H1 (LIVRNOT03)
54	109	399337 7	LUNGNON03	3003233H1 (TLYMNOT06), 3993377H1 (LUNGNON03), 3993377T6 (LUNGNON03), 4251662F6 (BRADDIR01), SBSA02001V1
55	110	471793 6	BRAIHCT02	4717936F6 (BRAIHCT02), 4717936H1 (BRAIHCT02), 4717936T6 (BRAIHCT02)

TABLE 2

Polypeptide Seq ID NO:	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequence(s)	Identification/ Homologous Sequence	Analytical Methods and Databases
1	754	S6 T15 S22 S26 S28 S30 S60 Y84 S98 S102 S103 S112 S121 S146 T166 T183 T184 S231 Y253 S303 T304 S308 T327 T361 T393 T394 T399 T448 S496 Y583 S586 T608 S635 S672 S673 S682 S691 S711 S713 S751		L435 - P474 PFAM	DNA polymerase	PFAM, BLOCKS, MOTIFS
2	593	S32 Y62 T65 S83 S141 T159 T160 S185 S254 S288 T311 S314 S333 T368 S380 S401 T410 S426 S452 S461 S479 T483 T485 T576		E102 - A157 Q201 - C252	PHD finger DNA binding protein (GI 3342452)	BLAST, PFAM, MOTIFS
3	534	T39 S52 S301 T344 S373 T404 S425 S438 S439 S440 S473 T480 S490 T527		I17 - D57 PFAM	DNA polymerase	PFAM, BLOCKS, MOTIFS
4	255	S10 S26 Y35 Y113 S149 T168 Y169 T248		Y58 - C86 F141 - H163 Y169 - H191 Y197 - H219 Y225 - H247 PFAM	C2H2-type zinc finger protein (GI 498721)	BLAST, PFAM, BLOCKS, PRINTS, MOTIFS

TABLE 2 (cont.)

Polypeptide Seq ID NO:	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequence(s)	Identification/ Homologous Sequence	Analytical Methods and Databases
5	562	T29 T43 S76 S142 S165 S202 T214 Y302 S305 Y349 S385 S500 T526 S527		Y235 - D312 PFAM	DNA helicase (GI 531243; SEQ ID NO:113)	BLAST, PFAM, BLOCKS, MOTIFS
6	432	S33 S58 T166 T172 S197 T230 T261 S275 S286 S290 S298 S338 T362 S376 T407 T409 T419		E329 - A355 BLOCKS	CCAAT-box-binding transcription factor	BLOCKS, MOTIFS
7	799	T24 S33 T43 S73 T88 S91 S110 S147 T219 S262 S323 Y380 S532 S586 S756 T795		H250 - H291 Y324 - H346 Y253 - H374 Y380 - H402 PFAM	C2H2-type zinc finger protein (GI 498727)	BLAST, PFAM, BLOCKS, PRINTS, MOTIFS
8	137	S3 T38 S74 S75 S118		R85 - L97 PFAM	BTB domain/C2H2-type zinc finger protein	PFAM, PRINTS, MOTIFS
9	230	T178 S187			sirtuin type 3 (GI 5225322)	BLAST, MOTIFS
10	446	T3 S28 S32 T52 T94 T96 S135 S143 T159 T165 S171 S433		H200 - H222 Y228 - H250 Y256 - H278 Y284 - H306	zinc finger protein ZFP113 (GI 5640017)	BLAST, PFAM, BLOCKS, PRINTS, MOTIFS
11	428	S72 S92 S101 S118 S120 S125 T245 T277 S289 S315 S317 Y326 S409			Skeletal muscle BOP2 (GI 5870834; SEQ ID NO:117)	BLAST, MOTIFS

TABLE 2 (cont.)

Polypeptide Seq ID No:	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequence(s)	Identification/ Homologous Sequence	Analytical Methods and Databases
12	590	S45 Y52 T60 S83 S90 T95 T116 T145 T233 T330 S391 S410 S411 T420 T439 T490 S521			Methyl-CpG binding protein (GI 2239126)	BLAST, MOTIFS
13	479	S15 Y29 S30 S118 T173 T183 S203 S217 Y232 S235 T255 S352 S362 Y451		Y232 - H254 H283 - H305 Y311 - H333 Y339 - H361 PFAM	SRE-ZBP (GI 936603)	BLAST, PFAM, BLOCKS, PRINTS, MOTIFS
14	433	S92 S96 T250 S319 T322 T327 S335 T344		C380 - C421 PFAM	C3HC4-type zinc finger protein	PFAM, BLOCKS, MOTIFS
15	320	T6 S27 T125 T172 S229 S232 T239 S248 S259 S266 Y267 S291			Zinc finger factor (GI 3150148)	BLAST, MOTIFS
16	179	S11 T21 S46 S140			Single-stranded DNA binding protein (csdp) (GI 1562534)	BLAST, MOTIFS
17	494	T73 Y80 S104 Y116 T192 S289 S297 T329 T364 T376 S387		C13 - H41 BLOCKS	Zinc finger transcription factor (GI 2895870)	BLAST, BLOCKS, MOTIFS
18	401	S4 S82 S97 T166 S188 S249 S279 S289 S290 S294 S319 S368 S371 S372 S378 T392 S396		P5 - K81 A114 - S179 G186 - P262 PFAM	HP1-BP74 (GI 1480112)	PFAM, BLOCKS, PRINTS, MOTIFS

TABLE 2 (cont.)

Polypeptide Seq ID NO:	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequence(s)	Identification/ Homologous Sequence	Analytical Methods and Databases
19	264	S11 S25 S76 S82 S90 S92 S96 S119 T229		F154 - H176 C180 - H202 F208 - H230 Y236 - C259 PFAM	C2H2-type zinc finger protein (GI 429188)	BLAST, PFAM, BLOCKS, PRINTS, MOTIFS
20	153	T23 S40 T44 S110 S120 T124		R42 - E141 PFAM	High mobility group-like nuclear protein (GI 2822179)	BLAST, PFAM, BLOCKS, PRINTS, MOTIFS
21	243	S20 S21 S76 S100 S104 S160 T194 S196 S212 T222 Y229		Y90 - H112 H118 - H140 Y146 - H168 Y174 - H195 PFAM	C2H2-type zinc finger protein (GI 38015)	BLAST, PFAM, BLOCKS, PRINTS, MOTIFS
22	485	T29 S34 S104 S147 T162 T248 S249 S256 S347 S452 S477		S309 - H331 H337 - H359 Y365 - H387 Y393 - H415 PFAM	BTB domain/C2H2-type zinc finger protein (GI 2843171)	BLAST, PFAM, BLOCKS, PRINTS, MOTIFS
23	160	S118		C5 - F62 C80 - F137 PFAM	LIM domain protein/CRP2 (GI 487284)	BLAST, PFAM, BLOCKS, PROFILES, MOTIFS
24	511	S10 T36 S75 S90 S222 T245 T259 S399 S405 Y443 S500		Y171 - P223 Y267 - K294 BLOCKS	2'-5' oligoadenylate synthetase-related protein p56 (GI 4731857)	BLOCKS, MOTIFS
25	310	S24 S39 T69 Y104 S185 T282 T296			SIR2 family transcriptional regulatory protein (GI 2648874)	BLAST, MOTIFS

TABLE 2 (cont.)

Polypeptide Seq ID NO:	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequence(s)	Identification/ Homologous Sequence	Analytical Methods and Databases
26	331	T29 S40 S74 S257 T270 S301		V112 - R134 BLOCKS	Histone protein	BLOCKS, MOTIFS
27	200	T43 S123 T129 S167 S183 S184			Zinc finger protein (g1373394)	MOTIFS BLAST
28	100	S44 Y25 Y98		Transcription anti-terminator; bglG family: E47-I100	transcription elongation factor (g4336506)	MOTIFS BLAST BLOCKS
29	528	S204 T487 S29 S34 T48 T227 S327 T367 T423 S483 Y39 Y44 Y112 Y163	N24 N52 N100 N481	C2H2 zinc fingers: Y191-H213 Y247-H269 Y275-H297 Y331-H353 Y387-H409 Y415-H437 Y443-H465 Y471-H493	Zinc finger protein (g498721)	MOTIFS BLAST BLOCKS PFAM
30	350	T264 S305	N33 N79	C3HC4 RING finger: C230-C271	C3HC4/RING zinc finger protein (g1321818)	MOTIFS BLAST BLOCKS PFAM PROFILES SCAN
31	315	S51 T94 S121 S123 S142 S143 T184 S232 S252 T36 T46 S159 S163 S168			Similar to CCAAT/enhancer-binding protein (g1947129)	MOTIFS BLAST
32	120	S36 S56 T93 S104	N98 N103	bZIP transcription factor: P21-P85		MOTIFS PFAM BLOCKS

TABLE 2 (cont.)

Polypeptide Seq ID NO:	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequence(s)	Identification/ Homologous Sequence	Analytical Methods and Databases
33	326	S59 S38 T207 S284 T319 T43 S80 T137 T155 T211 S238 T239	N209	C2H2 zinc fingers: C143-C171 Y169-H191 F197-H219	Zinc finger protein (g220643)	MOTIFS BLAST PFAM BLOCKS
34	106	S80 T89 T39 T53		Homeobox: R14-K70	CHOX M product; homeobox protein (g62701)	MOTIFS BLAST BLOCKS PFAM PROFILES SCAN
35	209	S176 T180 S184 T193 S201 S4 T25 S49	N18	bZIP transcription factor: K115-E140	geminin (g3219357)	MOTIFS BLAST PFAM
36	212	S79 S107 T127 T202 S45 S56 S124 T152 Y35	N92	HMG box: M1-Q36	Smadcell-related protein (GI 4321968)	MOTIFS BLAST PFAM
37	359	T329 T50 S125 S224 S230 S235 S344 S31 S215 S312 Y42	N45 N340	C2H2 zinc fingers: F278-C306 Y304-H328 F334-H356	BKLF; CACCC-box binding protein (g1244515)	MOTIFS BLAST BLOCKS PFAM
38	445	S68 T87 S153 S339 S405 S55 T105 S315 S422 Y419	N337 N374 N388	C3HC4 RING fingers: C74-P120 N228-C235	ARI (RING finger) protein (g2058299)	MOTIFS BLAST BLOCKS PFAM
39	433	S283 T44 T57 T123 S136 T185 T220 S239 T268 S313 S330 T105 T109 S125 T216	N169 N206		skm-BOP2 zinc finger protein (g1809327)	MOTIFS BLAST

TABLE 2 (cont.)

Polypeptide Seq ID NO:	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequence(s)	Identification/ Homologous Sequence	Analytical Methods and Databases
40	355	T72 T84 T184 S191 T244 S88 T162 T229 T294 S330	N308 N324		Sir2 family protein (g5353746)	MOTIFS BLAST
41	443	T76 T106 S148 T309 S12 T253 S299 S357 T373 T427 Y61 Y114	N366 N425	Myb-like DNA binding domain: D72-F118	ADA2 transcriptional adaptor protein (g170991)	MOTIFS BLAST BLOCKS PFAM PROFILES SCAN
42	164	S37 T55 T64 S83 S22 Y146	N117	mutT domain: V29-L70		MOTIFS BLOCKS PFAM
43	215	S79 S127 T12 T45		HMG box: M1-Q36	Sry-related protein (g211510)	MOTIFS BLAST PFAM
44	539	T15 S24 S66 S83 T97 T105 T109 S128 T149 S153 S198 T203 T225 T238 T296 S466 Y258	N465	C2H2 zinc fingers: H230-H252 Y258-H280 Y286-H308 Y314-H336 Y342-H364 F370-H392 Y398-H420 Y426-H448 Y482-H504 Y510-H532	C2H2 zinc finger protein (g5757625)	MOTIFS BLAST PFAM BLOCKS
45	182	T59 S112 S120 S100 S139 Y64			Transcriptional regulator (g2621798)	MOTIFS BLAST

TABLE 2 (cont.)

Polypeptide Seq ID NO:	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequence(s)	Identification/ Homologous Sequence	Analytical Methods and Databases
46	534	S494 S31 S44 S117 T123 S185 S216 S476 S504 S176 S182 S211 T249 S293 S323 S409 T489 Y76 Y285	N29 N39 N250 N351	C2H2 zinc fingers: Y285-H307 Y313-H335 Y341-H363 C369-H391 Y397-H419 Y425-H447 Y453-H475 Y481-H503 Y509-H531	Zinc finger protein (g1373394)	MOTIFS BLAST PFAM BLOCKS
47	206	S5 S7 S40 S45 S46 S100 S144 S26 S107 T148 S185 Y38	N44 N177	Myc-type HLH domain: Q108-R160	Musculin (g3599519)	MOTIFS BLAST PFAM BLOCKS PROFILES SCAN
48	172	T5 S87 S96 S115 T124 S22 T64			KRAB zinc finger protein (g1049295)	MOTIFS BLAST
49	275	S185 S14 S48 T54 S118 T139 T161 T189 T217 Y256	N210 N214 N238 N260	C2H2 zinc fingers: F172-H194 Y200-H222 Y228-H250	Repressor transcriptional factor (g1017722)	MOTIFS BLAST PFAM BLOCKS
50	236	S157 S42 T167 T222 T81 Y213	N40	C3HC4 RING finger: P126-L150	Ariadne-2 RING finger protein (g3445441)	MOTIFS BLAST BLOCKS
51	214	S7 S8 S116 T127 S154 S191 T31 S41 T204	N2	Chromodomain: V113-E134	Nucleoplasmin (g833629)	MOTIFS BLAST BLOCKS

TABLE 2 (cont.)

Polypeptide Seq ID NO:	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequence(s)	Identification/ Homologous Sequence	Analytical Methods and Databases
52	396	T348 T392 S118 T193 T201 S270 S294 S80 S112 S206 S260 T313 T355 S375 S387	N2	C3HC4 RING finger: C26-C50	Midline 1/ cerebellar isoform 1 RING finger protein (g3462503)	MOTIFS BLAST PFAM BLOCKS PROFILES SCAN
53	486	S29 T58 S155 S239 T292 T379 S146 T271 S425			5'-nucleotidase (g633071)	MOTIFS BLAST
54	555	S432 T502 S68 S195 T199 T226 S315 T379 T441 T534 S170 S248 S282 S291 T327 T336 S391 S422 T481 Y257 Y274	N25 N66 N246 N364	ATP/GTP binding site (P-loop): A434-T441	Transcription termination factor I (TTF-I) interacting peptide 5 isoform (g2183083)	MOTIFS BLAST
55	61	T34 T42 Y48			Putative leucine-rich DNA-binding protein (g555991)	MOTIFS BLAST

TABLE 3

Nucleotide Seq ID NO:	Selected Fragment	Tissue Expression (Fraction of Total)	Disease or Condition (Fraction of Total)	Vector
56	169-215	Reproductive (0.224) Nervous (0.198) Cardiovascular (0.112)	Cell Proliferative (0.725) Inflammation (0.190)	PBLUESCRIPT
57	551-595	Hematopoietic/Immune (0.240) Reproductive (0.180) Gastrointestinal (0.120)	Cell Proliferative (0.700) Inflammation (0.360)	PBLUESCRIPT
58	541-585	Nervous (0.286) Reproductive (0.286) Cardiovascular (0.214)	Cell Proliferative (0.643) Trauma (0.214)	PBLUESCRIPT
59	109-153	Reproductive (1.000)	Cell Proliferative (1.000) Inflammation (1.000)	PBLUESCRIPT
60	435-479	Hematopoietic/Immune (0.211) Gastrointestinal (0.183) Reproductive (0.183)	Cell Proliferative (0.620) Inflammation (0.338)	PBLUESCRIPT
61	1195-1239	Reproductive (0.248) Cardiovascular (0.174) Nervous (0.157)	Cell Proliferative (0.637) Inflammation (0.256)	PBLUESCRIPT
62	217-261	Reproductive (0.429) Nervous (0.238) Cardiovascular (0.095)	Cell Proliferative (0.667) Inflammation (0.143) Trauma (0.095)	PBLUESCRIPT
63	919-963	Reproductive (0.265) Nervous (0.235) Cardiovascular (0.088)	Cell Proliferative (0.618) Inflammation (0.206)	PSPORT1
64	823-876	Reproductive (0.382) Nervous (0.176) Gastrointestinal (0.118)	Cell Proliferative (0.794)	PSPORT1
65	380-424	Reproductive (0.346) Nervous (0.154) Gastrointestinal (0.135)	Cell Proliferative (0.750) Inflammation (0.231)	PSPORT1

TABLE 3 (cont.)

Nucleotide Seq ID NO:	Selected Fragment	Tissue Expression (Fraction of Total)	Disease or Condition (Fraction of Total)	Vector
66	757-801	Nervous (0.222) Hematopoietic/Immune (0.167) Reproductive (0.167)	Cell Proliferative (0.778) Inflammation (0.222)	pINCY
67	812-856	Reproductive (0.246) Nervous (0.180) Gastrointestinal (0.148)	Cell Proliferative (0.639) Inflammation (0.246)	pINCY
68	326-370	Reproductive (0.500) Nervous (0.200) Gastrointestinal (0.150)	Cell Proliferative (0.700) Trauma (0.150)	pINCY
69	703-747	Reproductive (0.278) Hematopoietic/Immune (0.204) Nervous (0.148)	Cell Proliferative (0.777) Inflammation (0.222)	pINCY
70	759-803	Reproductive (0.261) Gastrointestinal (0.217) Nervous (0.174)	Cell Proliferative (0.565) Trauma (0.130)	pINCY
71	110-154	Nervous (0.250) Developmental (0.208) Gastrointestinal (0.167)	Cell Proliferative (0.583) Trauma (0.167)	pINCY
72	529-573	Reproductive (0.186) Gastrointestinal (0.168) Hematopoietic/Immune (0.138)	Cell Proliferative (0.700) Inflammation (0.251)	pINCY
73	1784-1828	Reproductive (0.286) Hematopoietic/Immune (0.190) Nervous (0.167)	Cell Proliferative (0.667) Inflammation (0.286)	PSPORT1
74	111-155	Reproductive (0.316) Nervous (0.211) Hematopoietic/Immune (0.158)	Cell Proliferative (0.632) Inflammation (0.211)	PSPORT1
75	543-587	Reproductive (0.258) Nervous (0.206) Gastrointestinal (0.134)	Cell Proliferative (0.608) Inflammation (0.196)	pINCY

TABLE 3 (cont.)

Nucleotide Seq ID NO:	Selected Fragment	Tissue Expression (Fraction of Total)	Disease or Condition (Fraction of Total)	Vector
76	272-316	Reproductive (0.246) Nervous (0.180) Hematopoietic/Immune (0.148)	Cell Proliferative (0.606) Inflammation (0.279)	pINCY
77	227-271	Hematopoietic/Immune (0.222) Endocrine (0.167) Cardiovascular (0.111)	Cell Proliferative (0.666) Inflammation (0.333)	pINCY
78	487-531	Gastrointestinal (0.375) Reproductive (0.250)	Cell Proliferative (0.500) Inflammation (0.250)	pINCY
79	111-155	Gastrointestinal (0.280) Hematopoietic/Immune (0.240) Reproductive (0.120)	Cell Proliferative (0.640) Inflammation (0.440)	pINCY
80	595-639	Reproductive (0.211) Gastrointestinal (0.158) Urologic (0.158)	Cell Proliferative (0.684) Inflammation (0.263)	pINCY
81	425-469	Reproductive (0.222) Gastrointestinal (0.160) Nervous (0.148)	Cell Proliferative (0.568) Inflammation (0.259)	PSPORT1
82	774-818	Gastrointestinal (0.200) Hematopoietic/Immune (0.200) Nervous (0.200)	Cancer (0.600) Trauma (0.200) Inflammation (0.200)	PBLUESCRIPT
83	517-561	Nervous (0.526) Reproductive (0.132) Cardiovascular (0.105)	Cancer (0.342) Fetal (0.158) Inflammation (0.158)	PBLUESCRIPT
84	1944-1988	Nervous (0.250) Reproductive (0.188) Endocrine (0.125)	Cancer (0.438) Fetal (0.250) Trauma (0.250)	PSPORT1
85	1027-1071	Reproductive (0.219) Nervous (0.206) Hematopoietic/Immune (0.116)	Cancer (0.458) Inflammation (0.232) Fetal (0.181)	PSPORT1

TABLE 3 (cont.)

Nucleotide Seq ID NO:	Selected Fragment	Tissue Expression (Fraction of Total)	Disease or Condition (Fraction of Total)	Vector
86	658-702	Reproductive (0.227) Hematopoietic/Immune (0.182) Gastrointestinal (0.167)	Cancer (0.424) Inflammation (0.318) Fetal (0.167)	PT7T3
87	488-532	Nervous (0.200) Reproductive (0.200) Musculoskeletal (0.120)	Cancer (0.320) Fetal (0.320) Inflammation (0.320)	pINCY
88	379-423	Cardiovascular (0.250) Nervous (0.250) Reproductive (0.250)	Cancer (0.417) Fetal (0.167) Neurological (0.167)	pINCY
89	632-676	Reproductive (0.417) Cardiovascular (0.167) Gastrointestinal (0.167)	Cancer (0.333) Fetal (0.167) Inflammation (0.167)	pINCY
90	258-302	Reproductive (0.294) Nervous (0.137) Hematopoietic/Immune (0.118)	Cancer (0.569) Fetal (0.431) Inflammation (0.176)	pINCY
91	433-477	Reproductive (0.750) Nervous (0.250)	Cancer (0.500) Inflammation (0.500)	PSPORT1
92	542-586	Gastrointestinal (0.273) Hematopoietic/Immune (0.273) Developmental (0.182)	Cancer (0.455) Inflammation (0.364) Fetal (0.182)	pINCY
93	218-262	Reproductive (0.272) Nervous (0.204) Cardiovascular (0.126)	Cancer (0.447) Inflammation (0.214) Fetal (0.155)	PSPORT1
94	541-585	Reproductive (0.273) Nervous (0.250) Cardiovascular (0.159)	Cancer (0.364) Fetal (0.205) Inflammation (0.205)	PSPORT1
95	111-155	Reproductive (0.250) Gastrointestinal (0.173) Nervous (0.154)	Cancer (0.481) Fetal (0.231) Inflammation (0.212)	PSPORT1
96	597-641	Reproductive (0.261) Cardiovascular (0.217) Nervous (0.130)	Cancer (0.391) Fetal (0.304) Inflammation (0.130)	PSPORT1

TABLE 3 (cont.)

Nucleotide Seq ID NO:	Selected Fragment	Tissue Expression (Fraction of Total)	Disease or Condition (Fraction of Total)	Vector
97	434-478	Cardiovascular (0.222) Endocrine (0.222) Gastrointestinal (0.222)	Cancer (0.667) Fetal (0.111) Neurological (0.111)	PSPORT1
98	218-247 920-964	Reproductive (0.333) Gastrointestinal (0.129) Hematopoietic/Immune (0.118)	Cancer (0.559) Inflammation (0.204) Fetal (0.183)	pINCY
99	327-371	Gastrointestinal (0.211) Reproductive (0.211) Cardiovascular (0.158)	Cancer (0.421) Fetal (0.316) Inflammation (0.158)	pINCY
100	596-625	Reproductive (0.230) Nervous (0.164) Gastrointestinal (0.131)	Cancer (0.590) Inflammation (0.246) Fetal (0.082)	PSPORT
101	487-531	Cardiovascular (0.235) Reproductive (0.235) Hematopoietic/Immune (0.176)	Cancer (0.588) Inflammation (0.176) Trauma (0.118)	pINCY
102	218-247 542-586	Gastrointestinal (0.241) Hematopoietic/Immune (0.207) Cardiovascular (0.138)	Cancer (0.448) Fetal (0.276) Inflammation (0.276)	pINCY
103	219-263	Reproductive (0.500) Cardiovascular (0.250) Hematopoietic/Immune (0.250)	Cancer (0.500) Inflammation (0.250) Trauma (0.250)	pINCY
104	111-140 327-371	Hematopoietic/Immune (0.286) Nervous (0.238) Reproductive (0.143)	Cancer (0.333) Fetal (0.286) Inflammation (0.286)	pINCY
105	243-281	Musculoskeletal (0.286) Nervous (0.286) Gastrointestinal (0.143)	Inflammation (0.429) Fetal (0.286) Cancer (0.286)	pINCY
106	271-315	Nervous (0.800) Reproductive (0.100) Cardiovascular (0.100)	Cancer (0.400) Inflammation (0.200) Trauma (0.200)	pINCY

TABLE 3 (cont.)

Nucleotide Seq ID NO:	Selected Fragment	Tissue Expression (Fraction of Total)	Disease or Condition (Fraction of Total)	Vector
107	489-533	Cardiovascular (0.364) Gastrointestinal (0.182) Reproductive (0.182)	Cancer (0.273) Trauma (0.273) Inflammation (0.182)	pINCY
108	156-200	Nervous (0.256) Reproductive (0.256) Hematopoietic/Immune (0.128)	Cancer (0.465) Fetal (0.291) Inflammation (0.186)	pINCY
109	1459-1503	Cardiovascular (0.250) Hematopoietic/Immune (0.250) Nervous (0.167)	Inflammation (0.417) Cancer (0.333) Trauma (0.167)	PSPORT1
110	164-208	Nervous (1.000)	Neurological (1.000)	pINCY

TABLE 4

Nucleotide SEQ ID NO:	Library	Library Comment
56	SPINFETO 1	Library was constructed at Stratagene, using RNA isolated from a pool of fetal spleen tissue. Following vector packaging, 2×10^6 primary clones were then amplified to stabilize the library for long-term storage. Amplification may significantly skew sequence abundances.
57	SYNORAB0 1	Library was constructed using RNA isolated from the synovial membrane tissue of a 68-year-old Caucasian female with rheumatoid arthritis.
58	KIDNNOTO 1	Library was constructed using RNA isolated from the kidney tissue of a 64-year-old Caucasian female, who died from an intracranial bleed. Patient history included rheumatoid arthritis and tobacco use.
59	PLACNOB0 1	Library was constructed using RNA isolated from placenta.
60	HNT2RAT0 1	Library was constructed at Stratagene (STR937231), using RNA isolated from the hNT2 cell line (derived from a human teratocarcinoma that exhibited properties characteristic of a committed neuronal precursor). Cells were treated with retinoic acid for 24 hours.
61	EOSIHETO 2	Library was constructed using RNA isolated from peripheral blood cells apheresed from a 48-year-old Caucasian male. Patient history included hypereosinophilia. The cell population was determined to be greater than 77% eosinophils by Wright's staining.
62	HNT2AGT0 1	Library was constructed at Stratagene (STR937233), using RNA isolated from the hNT2 cell line (derived from a human teratocarcinoma that exhibited properties characteristic of a committed neuronal precursor). Cells were treated with retinoic acid for 5 weeks and with mitotic inhibitors for two weeks and allowed to mature for an additional 4 weeks in conditioned medium.
63	PROSNOTO 2	Library was constructed using RNA isolated from the diseased prostate tissue removed from a 50-year-old Caucasian male during a retropubic prostatectomy. Pathology indicated adenofibromatous hyperplasia was present. Pathology for the associated tumor tissue indicated adenocarcinoma Gleason grade 3+3. Patient history included dysuria, carcinoma in situ of prostate, coronary atherosclerosis, and hyperlipidemia.
64	COLNTUTO 2	Library was constructed using RNA isolated from colon tumor tissue removed from a 75-year-old Caucasian male during a hemicolectomy. Pathology indicated invasive grade 3 adenocarcinoma arising in a tubulovillous adenoma, which was distal to the ileocecal valve in the cecum. The tumor penetrated deeply into the muscularis propria but not through it.

TABLE 4 (cont.)

Nucleotide SEQ ID NO:	Library	Library Comment
65	KIDNTUTO 1	Library was constructed using RNA isolated from the kidney tumor tissue removed from an 8-month-old female during nephroureterectomy. Pathology indicated Wilms' tumor (nephroblastoma), which involved 90 percent of the renal parenchyma. Prior to surgery, the patient was receiving heparin anticoagulant therapy.
66	THYRNOTO 3	Library was constructed using RNA isolated from thyroid tissue removed from the left thyroid of a 28-year-old Caucasian female during a complete thyroidectomy. Pathology indicated a small nodule of adenomatous hyperplasia present in the left thyroid. Pathology for the associated tumor tissue indicated dominant follicular adenoma, forming a well-encapsulated mass in the left thyroid.
67	BLADTUTO 4	Library was constructed using RNA isolated from bladder tumor tissue removed from a 60-year-old Caucasian male during a radical cystectomy, prostatectomy, and vasectomy. Pathology indicated grade 3 transitional cell carcinoma in the left bladder wall. Carcinoma in-situ was identified in the dome and trigone. Patient history included tobacco use. Family history included type I diabetes, a malignant neoplasm of the stomach, atherosclerotic coronary artery disease, and an acute myocardial infarction.
68	PROSNOT1 5	Library was constructed using RNA isolated from diseased prostate tissue removed from a 66-year-old Caucasian male during radical prostatectomy and regional lymph node excision. Pathology indicated adenofibromatous hyperplasia. Pathology for the associated tumor tissue indicated an adenocarcinoma (Gleason grade 2+3). The patient presented with elevated prostate specific antigen (PSA). Family history included prostate cancer, secondary bone cancer, and benign hypertension.
69	BRSTTUTO 8	Library was constructed using RNA isolated from breast tumor tissue removed from a 45-year-old Caucasian female during unilateral extended simple mastectomy. Pathology indicated invasive nuclear grade 2-3 adenocarcinoma, ductal type, with 3 of 23 lymph nodes positive for metastatic disease. Greater than 50% of the tumor volume was in situ, both comedo and non-comedo types. Immunostains were positive for estrogen/progesterone receptors, and uninvolved tissue showed proliferative changes. The patient concurrently underwent a total abdominal hysterectomy. Patient history included valvuloplasty of mitral valve without replacement, rheumatic mitral insufficiency, and rheumatic heart disease. Family history included acute myocardial infarction, atherosclerotic coronary artery disease, and type II diabetes.

TABLE 4 (cont.)

Nucleotide SEQ ID NO:	Library	Library Comment
70	PROSNOT1 9	Library was constructed using RNA isolated from diseased prostate tissue removed from a 59-year-old Caucasian male during a radical prostatectomy with regional lymph node excision. Pathology indicated adenofibromatous hyperplasia. Pathology for the associated tumor tissue indicated an adenocarcinoma (Gleason grade 3+3). The patient presented with elevated prostate-specific antigen (PSA). Patient history included colon diverticuli, asbestosis, and thrombophlebitis. Previous surgeries included a partial colectomy. Family history included benign hypertension, multiple myeloma, hyperlipidemia and rheumatoid arthritis.
71	THPINOT0 3	Library was constructed using RNA isolated from untreated THP-1 cells. THP-1 (ATCC TIB 202) is a human promonocyte line derived from the peripheral blood of a 1-year-old Caucasian male with acute monocytic leukemia (ref: Int. J. Cancer (1980) 26:171).
72	THPINOT0 3	Library was constructed using RNA isolated from untreated THP-1 cells. THP-1 (ATCC TIB 202) is a human promonocyte line derived from the peripheral blood of a 1-year-old Caucasian male with acute monocytic leukemia (ref: Int. J. Cancer (1980) 26:171).
73	HIPAZT0 1	Library was constructed from RNA isolated from diseased hippocampus tissue removed from the brain of a 74-year-old Caucasian male who died from Alzheimer's disease.
74	HIPAZT0 1	Library was constructed from RNA isolated from diseased hippocampus tissue removed from the brain of a 74-year-old Caucasian male who died from Alzheimer's disease.
75	BRSTNOT1 3	Library was constructed using RNA isolated from breast tissue removed from the left medial lateral breast of a 36-year-old Caucasian female during bilateral simple mastectomy and total breast reconstruction. Pathology indicated benign breast tissue. Patient history included a breast neoplasm, depressive disorder, hyperlipidemia, chronic stomach ulcer, and an ectopic pregnancy. Family history included myocardial infarction, cerebrovascular disease, atherosclerotic coronary artery disease, hyperlipidemia, skin cancer, breast cancer, depressive disorder, esophageal cancer, bone cancer, Hodgkin's lymphoma, bladder cancer, and heart condition.
76	NPOLNOT0 1	Library was constructed using RNA isolated from nasal polyp tissue removed from a 78-year-old Caucasian male during a nasal polypectomy. Pathology indicated a nasal polyp and striking eosinophilia. Patient history included asthma and nasal polyps.

TABLE 4 (cont.)

Nucleotide SEQ ID NO:	Library	Library Comment
77	ADRENOTO 9	Library was constructed using RNA isolated from left adrenal gland tissue removed from a 43-year-old Caucasian male during nephroureterectomy, regional lymph node excision, and unilateral left adrenalectomy. Pathology indicated no diagnostic abnormalities of the adrenal gland. Pathology for the associated tumor tissue indicated a grade 2 renal cell carcinoma mass in the posterior lower pole of the left kidney with invasion into the renal pelvis.
78	SPLNNOT1 1	Library was constructed using RNA isolated from diseased spleen tissue removed from a 14-year-old Asian male during a total splenectomy. Pathology indicated changes consistent with idiopathic thrombocytopenic purpura. The patient presented with bruising.
79	CONCNOT0 1	Library was constructed using RNA isolated from chest wall soft tissue removed from a 63-year-old Caucasian male during a chest wall lesion destruction. Pathology indicated surgical margins were free of tumor. Pathology for the associated tumor tissue indicated invasive grade 3 adenocarcinoma, forming a mass that extended through the visceral pleura to involve parietal pleura. Patient history included MEN (multiple endocrine neoplasia) syndrome type I, abnormal secretion of gastrin, alcohol and tobacco abuse, calcium metabolism disease, chronic stomach ulcer with hemorrhage, lung cancer, and calculus of the kidney. Family history included prostate cancer, benign hypertension, stroke, atherosclerotic coronary artery disease, type II diabetes, hyperlipidemia, and cancer of an unspecified location.
80	TONSNOTO 3	Library was constructed using RNA isolated from diseased left tonsil tissue removed from a 6-year-old Caucasian male during adenotonsillectomy. Pathology indicated reactive lymphoid hyperplasia, bilaterally. Family history included benign hypertension, myocardial infarction, and atherosclerotic coronary artery disease.
81	LUNGNONO 3	This normalized library was constructed from 2.56×10^6 independent clones from a lung tissue library. RNA was made from lung tissue removed from the left lobe a 58-year-old Caucasian male during a segmental lung resection. Pathology for the associated tumor tissue indicated a metastatic grade 3 (of 4) osteosarcoma. Patient history included soft tissue cancer, secondary cancer of the lung, prostate cancer, and an acute duodenal ulcer with hemorrhage. Patient also received radiation therapy to the retroperitoneum. Family history included prostate cancer, breast cancer, and acute leukemia. The normalization and hybridization conditions were adapted from Soares et al., PNAS (1994) 91:9228; Swaroop et al., NAR (1991) 19:1954; and Bonaldo et al., Genome Research (1996) 6:791.

TABLE 4 (cont.)

Nucleotide SEQ ID NO:	Library	Library Comment
82	BMARNOT0 2	The library was constructed using Clontech RNA isolated from the bone marrow of 24 male and female Caucasian donors, 16 to 70 years old.
83	SINTNOT0 2	The library was constructed using RNA isolated from the small intestine of a 55-year-old Caucasian female, who died from a subarachnoid hemorrhage. Serologies were positive for cytomegalovirus (CMV).
84	CRBLNOT0 1	The library was constructed using RNA isolated from the cerebellum tissue of a 69-year-old Caucasian male who died from chronic obstructive pulmonary disease. Patient history included myocardial infarction, hypertension, and osteoarthritis.
85	BRSTNOT0 3	The library was constructed using RNA isolated from diseased breast tissue removed from a 54-year-old Caucasian female during a bilateral radical mastectomy. Pathology for the associated tumor tissue indicated residual invasive grade 3 mammary ductal adenocarcinoma. Patient history included kidney infection and condyloma acuminatum. Family history included benign hypertension, hyperlipidemia and a malignant neoplasm of the colon.
86	BEPINOT0 1	The normalized bronchial epithelium library was constructed from 5.12 million independent clones from a bronchial epithelium library. RNA was isolated from a bronchial epithelium primary cell line derived from a 54-year-old Caucasian male. The normalization and hybridization conditions were adapted from Soares et al., PNAS (1994) 91:9228, using a 24-hour reannealing hybridization period.
87	THYRNOT0 3	The library was constructed using RNA isolated from thyroid tissue removed from the left thyroid of a 28-year-old Caucasian female during a complete thyroidectomy. Pathology indicated a small nodule of adenomatous hyperplasia present in the left thyroid. Pathology for the associated tumor tissue indicated dominant follicular adenoma, forming a well-encapsulated mass in the left thyroid.
88	COLNFETO 2	The library was constructed using RNA isolated from the colon tissue of a Caucasian female fetus who died at 20 weeks' gestation.
89	BLADNOT0 3	The library was constructed using RNA isolated from bladder tissue removed from an 80-year-old Caucasian female during a radical cystectomy and lymph node excision. Pathology for the associated tumor tissue indicated grade 3 invasive transitional cell carcinoma. Patient history included malignant neoplasm of the uterus, atherosclerosis, and atrial fibrillation. Family history included acute renal failure, osteoarthritis, and atherosclerosis.

TABLE 4 (cont.)

Nucleotide SEQ ID NO:	Library	Library Comment
90	COLNNOT2 3	The library was constructed using RNA isolated from diseased colon tissue removed from a 16-year-old Caucasian male during a total colectomy with abdominal/perineal resection. Pathology indicated gastritis and pancolitis consistent with the acute phase of ulcerative colitis. Inflammation was more severe in the transverse colon with inflammation confined to the mucosa. The ascending and sigmoid colon was mildly involved. Family history included irritable bowel syndrome.
91	BRSTNOT0 4	The library was constructed using RNA isolated from breast tissue removed from a 62-year-old East Indian female during a unilateral extended simple mastectomy. Pathology for the associated tumor tissue indicated an invasive grade 3 ductal carcinoma. Patient history included benign hypertension, hyperlipidemia, and hematuria. Family history included cerebrovascular and cardiovascular disease, hyperlipidemia, and liver cancer.
92	LIVRFETO 2	The library was constructed using RNA isolated from liver tissue removed from a Caucasian female fetus who died at 20 weeks' gestation. Family history included seven days of erythromycin treatment for bronchitis in the mother during the first trimester.
93	BEPINOT0 1	The library was constructed using RNA isolated from a bronchial epithelium primary cell line derived from a 54-year-old Caucasian male.
94	BRAITUTO 2	The library was constructed using RNA isolated from brain tumor tissue removed from the frontal lobe of a 58-year-old Caucasian male during excision of a cerebral meningeal lesion. Pathology indicated a grade 2 metastatic hypernephroma. Patient history included a grade 2 renal cell carcinoma, insomnia, and chronic airway obstruction. Family history included a malignant neoplasm of the kidney.
95	BRAITUTO 3	The library was constructed using RNA isolated from brain tumor tissue removed from the left frontal lobe of a 17-year-old Caucasian female during excision of a cerebral meningeal lesion. Pathology indicated a grade 4 fibrillary giant and small-cell astrocytoma. Family history included benign hypertension and cerebrovascular disease.
96	BRSTTUTO 2	The library was constructed using RNA isolated from breast tumor tissue removed from a 54-year-old Caucasian female during a bilateral radical mastectomy with reconstruction. Pathology indicated residual invasive grade 3 mammary ductal adenocarcinoma. The remaining breast parenchyma exhibited proliferative fibrocystic changes without atypia. One of 10 axillary lymph nodes had metastatic tumor. Patient history included kidney infection and condyloma acuminatum. Family history included benign hypertension, hyperlipidemia, and a malignant colon neoplasm.

TABLE 4 (cont.)

Nucleotide SEQ ID NO:	Library	Library Comment
97	BRSTTUT0 2	The library was constructed using RNA isolated from breast tumor tissue removed from a 54-year-old Caucasian female during a bilateral radical mastectomy with reconstruction. Pathology indicated residual invasive grade 3 mammary ductal adenocarcinoma. The remaining breast parenchyma exhibited proliferative fibrocystic changes without atypia. One of 10 axillary lymph nodes had metastatic tumor. Patient history included kidney infection and condyloma acuminatum. Family history included benign hypertension, hyperlipidemia, and a malignant colon neoplasm.
98	BRSTNOT0 7	The library was constructed using RNA isolated from diseased breast tissue removed from a 43-year-old Caucasian female during a unilateral extended simple mastectomy. Pathology indicated mildly proliferative fibrocystic changes with epithelial hyperplasia, papillomatosis, and duct ectasia. Pathology for the associated tumor tissue indicated invasive grade 4, nuclear grade 3 mammary adenocarcinoma with extensive comedo necrosis. Family history included epilepsy, cardiovascular disease, and type II diabetes.
99	BRAINOT0 9	The library was constructed using RNA isolated from brain tissue removed from a Caucasian male fetus who died at 23 weeks' gestation.
100	THPIAZS0 8	The library was constructed using RNA isolated from 5.76 million clones from a 5-aza-2'-deoxycytidine treated THP-1 cell library. The library was subjected to subtractive hybridization using 5 million clones from an untreated THP-1 cell library. Hybridization conditions were adapted from Swaroop et al., NAR (1991) 19:1954; and Bonaldo et al., Genome Research (1996) 6:791. THP-1 (ATCC TIB 202) is a human promonocyte cell line derived from peripheral blood of a 1-year-old Caucasian male with acute monocytic leukemia.
101	LUNGUT1 2	The library was constructed using RNA isolated from tumorous lung tissue removed from a 70-year-old Caucasian female during a lung lobectomy of the left upper lobe. Pathology indicated grade 3 (of 4) adenocarcinoma and vascular invasion. Patient history included tobacco abuse, depressive disorder, anxiety state, and skin cancer. Family history included cerebrovascular disease, congestive heart failure, colon cancer, depressive disorder, and primary liver.
102	HEAONOT0 5	The library was constructed using RNA isolated from aortic tissue removed from a 17-year-old Hispanic female who died from a gunshot wound.
103	HEAONOT0 5	The library was constructed using RNA isolated from aortic tissue removed from a 17-year-old Hispanic female who died from a gunshot wound.

TABLE 4 (cont.)

Nucleotide SEQ ID NO:	Library	Library Comment
104	EPIGNOT0 1	The library was constructed using RNA isolated from epiglottic tissue removed from a 71-year-old male during laryngectomy with right parathyroid biopsy. Pathology for the associated tumor tissue indicated recurrent grade 1 papillary thyroid carcinoma.
105	CONCNOT0 1	The library was constructed using RNA isolated from chest wall soft tissue removed from a 63-year-old Caucasian male during a chest wall lesion destruction. Pathology for the associated tumor tissue indicated invasive grade 3 adenocarcinoma forming a mass that extended through the visceral pleura to involve parietal pleura. Patient history included multiple endocrine neoplasia syndrome type I, abnormal secretion of gastrin, alcohol and tobacco abuse, calcium metabolism disease, chronic stomach ulcer with hemorrhage, lung cancer, and calculus of the kidney. Family history included prostate cancer, benign hypertension, stroke, atherosclerotic coronary artery disease, type II diabetes, hyperlipidemia, and an unspecified cancer.
106	BRONNOT0 1	The library was constructed using RNA isolated from bronchial tissue removed from a 15-year-old Caucasian male.
107	BRONNOT0 1	The library was constructed using RNA isolated from bronchial tissue removed from a 15-year-old Caucasian male.
108	LIVRNOT0 3	The library was constructed using RNA isolated from liver tissue removed from a Caucasian male fetus who died from Patau's syndrome (trisomy 13) at 20 weeks' gestation.
109	LUNGNOT0 3	The normalized library was constructed from 2.56 million independent clones from a lung tissue library. RNA was isolated from lung tissue removed from the left lobe a 58-year-old Caucasian male during a segmental lung resection. Pathology for the associated tumor tissue indicated a metastatic grade 3 (of 4) osteosarcoma. Patient history included soft tissue cancer, secondary cancer of the lung, prostate cancer, acute duodenal ulcer with hemorrhage, and radiation therapy to the retroperitoneum. Family history included prostate cancer, breast cancer, and acute leukemia. The normalization and hybridization conditions were adapted from Soares et al., PNAS (1994) 91:9228; Swaroop et al., NAR (1991) 19:1954; and Bonaldo et al., Genome Research (1996) 6:791.
110	BRAIHT0 2	The library was constructed using RNA isolated from diseased choroid plexus tissue removed from the brain of a 57-year-old Caucasian male who died from a cerebrovascular accident. Patient history included Huntington's disease and emphysema.

Table 5

Program	Description	Reference	Parameter Threshold
ABI FACTURA	A program that removes vector sequences and masks ambiguous bases in nucleic acid sequences.	Perkin-Elmer Applied Biosystems, Foster City, CA.	
ABI/PARACEL PDF	A Fast Data Finder useful in comparing and annotating amino acid or nucleic acid sequences.	Perkin-Elmer Applied Biosystems, Foster City, CA; Paracel Inc., Pasadena, CA.	Mismatch <50%
ABI AutoAssembler	A program that assembles nucleic acid sequences.	Perkin-Elmer Applied Biosystems, Foster City, CA.	
BLAST	A Basic Local Alignment Search Tool useful in sequence similarity search for amino acid and nucleic acid sequences. BLAST includes five functions: blastp, blastn, blastx, tblastn, and tblastx.	Altschul, S.F. et al. (1990) J. Mol. Biol. 215:403-410; Altschul, S.F. et al. (1997) Nucleic Acids Res. 25: 3389-3402.	ESTs: Probability value= 1.0E-8 or less Full Length sequences: Probability value= 1.0E-10 or less
FASTA	A Pearson and Lipman algorithm that searches for similarity between a query sequence and a group of sequences of the same type. FASTA comprises at least five functions: fasta, tfasta, fastx, tfastx, and ssearch.	Pearson, W.R. and D.J. Lipman (1988) Proc. Natl. Acad. Sci. 85:2444-2448; Pearson, W.R. (1990) Methods Enzymol. 183: 63-98; and Smith, T.F. and M. S. Waterman (1981) Adv. Appl. Math. 2:482-489.	ESTs: fasta E value= 1.06E-6 Assembled ESTs: fasta Identity= 95% or greater and Match length=200 bases or greater. fastx E value= 1.0E-8 or less Full Length sequences: fastx score= 100 or greater
BLIMPS	A BLocks IMProved Searcher that matches a sequence against those in BLOCKS, PRINTS, DOMO, PRODOM, and PFAM databases to search for gene families, sequence homology, and structural fingerprint regions.	Henikoff, S. and J.G. Henikoff, Nucl. Acid Res., 19:6565-72, 1991. J.G. Henikoff and S. Henikoff (1996) Methods Enzymol. 266:88-105; and Attwood, T.K. et al. (1997) J. Chem. Inf. Comput. Sci. 37: 417-424.	Score= 1000 or greater; Ratio of Score/Strength = 0.75 or larger; and, if applicable, Probability value= 1.0E-3 or less
HIMMER	An algorithm for searching a query sequence against hidden Markov model (HMM)-based databases of protein family consensus sequences, such as PFAM.	Krogh, A. et al. (1994) J. Mol. Biol., 235:1501-1531; Sonnhammer, E.L.L. et al. (1988) Nucleic Acids Res. 26:320-322.	Score= 10-50 bits for PFAM hits, depending on individual protein families

Table 5 (cont.)

Program	Description	Reference	Parameter Threshold
ProfileScan	An algorithm that searches for structural and sequence motifs in protein sequences that match sequence patterns defined in Prosite.	Gribskov, M. et al. (1988) CABIOS 4:61-66; Gribskov, et al. (1989) Methods Enzymol. 183:146-159; Bairoch, A. et al. (1997) Nucleic Acids Res. 25: 217-221.	Normalized quality score \geq GCG-specified "HIGI" value for that particular Prosite motif. Generally, score=1.4-2.1.
Phred	A base-calling algorithm that examines automated sequencer traces with high sensitivity and probability.	Ewing, B. et al. (1998) Genome Res. 8:175-185; Ewing, B. and P. Green (1998) Genome Res. 8:186-194.	
Phrap	A Phils Revised Assembly Program including SWAT and CrossMatch, programs based on efficient implementation of the Smith-Waterman algorithm, useful in searching sequence homology and assembling DNA sequences.	Smith, T.F. and M. S. Waterman (1981) Adv. Appl. Math. 2:482-489; Smith, T.F. and M. S. Waterman (1981) J. Mol. Biol. 147:195-197; and Green, P., University of Washington, Seattle, WA.	Score= 120 or greater; Match length= 56 or greater
Consed	A graphical tool for viewing and editing Phrap assemblies	Gordon, D. et al. (1998) Genome Res. 8:195-202.	
SPScan	A weight matrix analysis program that scans protein sequences for the presence of secretory signal peptides.	Nielson, H. et al. (1997) Protein Engineering 10:1-6; Claverie, J.M. and S. Audic (1997) CABIOS 12: 431-439.	Score=3.5 or greater
Motifs	A program that searches amino acid sequences for patterns that matched those defined in Prosite.	Bairoch et al. <i>supra</i> ; Wisconsin Package Program Manual, version 9, page M51-59, Genetics Computer Group, Madison, WI.	

WO 00/44900

PCT/US00/02237

What is claimed is:

1. An isolated polypeptide comprising:

- a) an amino acid sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:3-5, SEQ ID NO:7-14, SEQ ID NO:16-31, SEQ ID NO:33-34, SEQ ID NO:36-40, SEQ ID NO:42-48, SEQ ID NO:50-55.
- b) a naturally occurring amino acid sequence having at least 90% sequence identity to an amino acid sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:3-5, SEQ ID NO:7-14, SEQ ID NO:16-31, SEQ ID NO:33-34, SEQ ID NO:36-40, SEQ ID NO:42-48, SEQ ID NO:50-55,
- c) a biologically active fragment of an amino acid sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:3-5, SEQ ID NO:7-14, SEQ ID NO:16-31, SEQ ID NO:33-34, SEQ ID NO:36-40, SEQ ID NO:42-48, SEQ ID NO:50-55, or
- d) an immunogenic fragment of an amino acid sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:3-5, SEQ ID NO:7-14, SEQ ID NO:16-31, SEQ ID NO:33-34, SEQ ID NO:36-40, SEQ ID NO:42-48, SEQ ID NO:50-55.

2. An isolated polypeptide of claim 1, having an amino acid sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:3-5, SEQ ID NO:7-14, SEQ ID NO:16-31, SEQ ID NO:33-34, SEQ ID NO:36-40, SEQ ID NO:42-48, SEQ ID NO:50-55.

3. An isolated polynucleotide encoding a polypeptide of claim 1.

4. An isolated polynucleotide of claim 3, having a sequence selected from the group consisting of SEQ ID NO:56-110.

5. A recombinant polynucleotide comprising a promoter sequence operably linked to a polynucleotide of claim 3.

6. A cell transformed with a recombinant polynucleotide of claim 5.

7. A transgenic organism comprising a polynucleotide of claim 5.

8. A method for producing a polypeptide of claim 1, the method comprising:

- a) culturing a cell under conditions suitable for expression of the polypeptide, wherein said

cell is transformed with a recombinant polynucleotide, and said recombinant polynucleotide comprises a promoter sequence operably linked to a polynucleotide encoding the polypeptide of claim 1, and

b) recovering the polypeptide so expressed.

5

9. An isolated antibody which specifically binds to a polypeptide of claim 1.

10. An isolated polynucleotide comprising:

10

a) a polynucleotide sequence selected from the group consisting of SEQ ID NO:56-110,

b) a naturally occurring polynucleotide sequence having at least 90% sequence identity to a polynucleotide sequence selected from the group consisting of SEQ ID NO:56-110,

c) a polynucleotide sequence complementary to a), or

d) a polynucleotide sequence complementary to b).

15

11. An isolated polynucleotide comprising at least 60 contiguous nucleotides of a polynucleotide of claim 10.

12. A method for detecting a target polynucleotide in a sample, said target polynucleotide having a sequence of a polynucleotide of claim 10, the method comprising:

20

a) hybridizing the sample with a probe comprising at least 16 contiguous nucleotides comprising a sequence complementary to said target polynucleotide in the sample, and which probe specifically hybridizes to said target polynucleotide, under conditions whereby a hybridization complex is formed between said probe and said target polynucleotide, and

25

b) detecting the presence or absence of said hybridization complex, and, optionally, if present, the amount thereof.

13. A method of claim 12, wherein the probe comprises at least 30 contiguous nucleotides.

30

14. A method of claim 12, wherein the probe comprises at least 60 contiguous nucleotides.

15. A pharmaceutical composition comprising an effective amount of a polypeptide of claim 1 and a pharmaceutically acceptable excipient.

35

16. A method of treating a disease or condition associated with decreased expression of

functional NuABP, comprising administering to a patient in need of such treatment the pharmaceutical composition of claim 15.

17. A method for screening a compound for effectiveness as an agonist of a polypeptide of
5 claim 1, the method comprising:

- a) exposing a sample comprising a polypeptide of claim 1 to a compound, and
- b) detecting agonist activity in the sample.

18. A pharmaceutical composition comprising an agonist compound identified by a method
10 of claim 17 and a pharmaceutically acceptable excipient.

19. A method of treating a disease or condition associated with decreased expression of functional NuABP, comprising administering to a patient in need of such treatment a pharmaceutical composition of claim 18.

15

20. A method for screening a compound for effectiveness as an antagonist of a polypeptide of claim 1, the method comprising:

- a) exposing a sample comprising a polypeptide of claim 1 to a compound, and
- b) detecting antagonist activity in the sample.

20

21. A pharmaceutical composition comprising an antagonist compound identified by a method of claim 20 and a pharmaceutically acceptable excipient.

22. A method for treating a disease or condition associated with overexpression of functional
25 NuABP, comprising administering to a patient in need of such treatment a pharmaceutical
composition of claim 21.

23. A method for screening a compound for effectiveness in altering expression of a target polynucleotide, wherein said target polynucleotide comprises a sequence of claim 4, the method comprising:

- exposing a sample comprising the target polynucleotide to a compound, and
- detecting altered expression of the target polynucleotide.

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau



(43) International Publication Date
3 August 2000 (03.08.2000)

PCT

(10) International Publication Number
WO 00/44900 A3

(51) International Patent Classification⁷: **C12N 15/12**,
C12Q 1/68, C07K 14/47, 16/18, G01N 33/68, A61K 38/17

(21) International Application Number: PCT/US00/02237

(22) International Filing Date: 28 January 2000 (28.01.2000)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
60/117,905 29 January 1999 (29.01.1999) US
60/117,904 29 January 1999 (29.01.1999) US

(63) Related by continuation (CON) or continuation-in-part
(CIP) to earlier applications:

US 60/117,904 (CIP)
Filed on 29 January 1999 (29.01.1999)
US 60/117,905 (CIP)
Filed on 29 January 1999 (29.01.1999)

(71) Applicant (for all designated States except US): **INCYTE
PHARMACEUTICALS, INC.** [US/US]; 3174 Porter
Drive, Palo Alto, CA 94304 (US).

(72) Inventors; and

(75) Inventors/Applicants (for US only): **TANG, Y., Tom**
[CN/US]; 4230 Ranwick Court, San Jose, CA 95118
(US). **LAL, Pretti** [IN/US]; 2382 Lass Drive, Santa Clara,
CA 95054 (US). **HILLMAN, Jennifer, L.** [US/US]; 230
Monrow Drive #12, Mountain View, CA 94040 (US).
YUE, Henry [US/US]; 826 Lois Avenue, Sunnyvale,
CA 94087 (US). **AZIMZAI, Yalda** [US/US]; 2045 Rock
Springs Drive, Hayward, CA 94545 (US). **LU, Aina,**
M., D. [US/US]; 55 Park Belmont Place, San Jose, CA
95136 (US). **BAUGHN, Mariah, R.** [US/US]; 14244

Santiago Road, San Leandro, CA 94577 (US). **TRAN,
Bao** [US/US]; 744 Kiely Boulevard, Santa Clara, CA
95051 (US). **SHIH, Leo, L.** [US/US]; Apartment B., 1081
Tanland Drive, Palo Alto, CA 94303 (US). **AU-YOUNG,
Janice, L.** [US/US]; 233 Golden Eagle Lane, Brisbane,
CA 94005 (US).

(74) Agents: **HAMLET-COX, Diana et al.**; Incyte Pharma-
ceuticals, Inc., 3174 Porter Drive, Palo Alto, CA 94304
(US).

(81) Designated States (*national*): AE, AL, AM, AT, AU, AZ,
BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE,
ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP,
KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD,
MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD,
SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ,
VN, YU, ZA, ZW.

(84) Designated States (*regional*): ARIPO patent (GH, GM,
KE, LS, MW, SD, SL, SZ, TZ, UG, ZW), Eurasian patent
(AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent
(AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU,
MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM,
GA, GN, GW, ML, MR, NE, SN, TD, TG).

Published:

- With international search report.
- Before the expiration of the time limit for amending the
claims and to be republished in the event of receipt of
amendments.

(88) Date of publication of the international search report:
30 November 2000

For two-letter codes and other abbreviations, refer to the "Guid-
ance Notes on Codes and Abbreviations" appearing at the begin-
ning of each regular issue of the PCT Gazette

(54) Title: NUCLEIC-ACID BINDING PROTEINS

(57) Abstract: The invention provides human nucleic-acid binding proteins (NuABP) and polynucleotides which identify and en-
code NuABP. The invention also provides expression vectors, host cells, antibodies, agonists, and antagonists. The invention also
provides methods for diagnosing, treating, or preventing disorders associated with expression of NuABP.

WO 00/44900 A3

Docket No.: PF-0662 USN

**DECLARATION AND POWER OF ATTORNEY FOR
UNITED STATES PATENT APPLICATION**

As a below named inventor, I hereby declare that:

My residence, post office address and citizenship are as stated below next to my name, and

I believe that I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if more than one name is listed below) of the subject matter which is claimed and for which a United States patent is sought on the invention entitled

NUCLEIC-ACID BINDING PROTEINS

the specification of which:

 / is attached hereto.

 / was filed on _____ as application Serial No. _____ and if this box contains an X /, was amended on _____.

 X / was filed as Patent Cooperation Treaty international application No. PCT/US00/02237 on January 28, 2000, this box contains an X /, was amended on under Patent Cooperation Treaty Article 19 on _____ 2001, and if this box contains an X /, was amended on _____.

I hereby state that I have reviewed and understand the contents of the above-identified specification, including the claims, as amended by any amendment referred to above.

I acknowledge my duty to disclose information which is material to the examination of this application in accordance with Title 37, Code of Federal Regulations, §1.56(a).

I hereby claim the benefit under Title 35, United States Code, §119 or §365(a)-(b) of any foreign application(s) for patent or inventor's certificate indicated below and of any Patent Cooperation Treaty international applications(s) designating at least one country other than the United States indicated below and have also identified below any foreign application(s) for patent or inventor's certificate and Patent Cooperation Treaty international application(s) designating at least one country other than the United States for the same subject matter and having a filing date before that of the application for said subject matter the priority of which is claimed:

Docket No.: PF-0662 USN

Country	Number	Filing Date	Priority Claimed
_____	_____	_____	// Yes // No
_____	_____	_____	// Yes // No

I hereby claim the benefit under Title 35, United States Code, §119(e) of any United States provisional application(s) listed below.

Application Serial No.	Filed	Status (Pending, Abandoned, Patented)
<u>60/117,905</u>	<u>January 29, 1999</u>	<u>Expired</u>
<u>60/117,904</u>	<u>January 29, 1999</u>	<u>Expired</u>

I hereby claim the benefit under Title 35, United States Code, §120 of any United States application(s) listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in said prior application(s) in the manner required by the first paragraph of Title 35, United States Code §112, I acknowledge my duty to disclose material information as defined in Title 37 Code of Federal Regulations, §1.56(a) which occurred between the filing date(s) of the prior application(s) and the national or Patent Cooperation Treaty international filing date of this application:

Application Serial No.	Filed	Status (Pending, Abandoned, Patented)
_____	_____	_____

I hereby appoint the following:

12

Lucy J. Billings	Reg. No. <u>36,749</u>
Michael C. Cerrone	Reg. No. <u>39,132</u>
Diana Hamlet-Cox	Reg. No. <u>33,302</u>
Richard C. Ekstrom	Reg. No. <u>37,027</u>
Barrie D. Greene	Reg. No. <u>46,740</u>
Lynn E. Murry	Reg. No. <u>42,918</u>
Shirley A. Recipon	Reg. No. <u>47,016</u>
Susan K. Sather	Reg. No. <u>44,316</u>
Michelle M. Stempien	Reg. No. <u>41,327</u>
David G. Streeter	Reg. No. <u>43,168</u>
Stephen Todd	Reg. No. <u>47,139</u>
P. Ben Wang	Reg. No. <u>41,420</u>

respectively and individually, as my patent attorneys and/or agents, with full power of substitution and revocation, to prosecute this application and to transact all business in the Patent and Trademark Office connected therewith. Please address all communications to:

Docket No.: PF-0662 USN

LEGAL DEPARTMENT
INCYTE GENOMICS, INC.
3160 PORTER DRIVE, PALO ALTO, CA 94304

TEL: 650-855-0555

FAX: 650-849-8886 or 650-845-4166

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issuing thereon.

First Joint Inventor:

1-00

Full name:

Y. Tom Tang

Signature:

[Signature]

Date:

Sept. 10, 2001

Citizenship

United States of America

Residence:

San Jose, California CA

P.O. Address:

4230 Ranwick Court
San Jose, California 95118**Second Joint Inventor:**

2-00

Full name:

Preeti Lal

Signature:

[Signature]

Date:

September 10, 2001

Citizenship

India

Residence:

Santa Clara, California CA

P.O. Address:

P.O. Box 5142
Santa Clara, California 95056

Docket No.: PF-0662 USN

3-00
Third Joint Inventor:

Full name:

Jennifer L. Hillman

Signature:

Jennifer L. Hillman

Date:

September 21, 2001

Citizenship

United States of America

Residence:

Mountain View, California CA

P.O. Address:

230 Monroe Drive, #17
Mountain View, California 940404-00
Fourth Joint Inventor:

Full name:

Henry Yue

Signature:

Henry Yue

Date:

September 24, 2001

Citizenship

United States of America

Residence:

Sunnyvale, California CA

P.O. Address:

826 Lois Avenue
Sunnyvale, California 940875-00
Fifth Joint Inventor:

Full name:

Yalda Azimzai

Signature:

Yalda Azimzai

Date:

September 13, 2001

Citizenship

United States of America

Residence:

Castro Valley, California CA

P.O. Address:

5518 Boulder Canyon Dr. Castro
Valley, California 94552

Docket No.: PF-0662 USN

6-00
Sixth Joint Inventor:

Full name: Dyung Aina M. Lu
Signature: *Aina Lu*
Date: Sept 7, 2001
Citizenship: United States of America
Residence: San Jose, California CA
P.O. Address: 233 Coy Drive
San Jose, California 95123

7-00
Seventh Joint Inventor:

Full name: Mariah R. Baughn
Signature: *Mariah R. Baughn*
Date: September 5, 2001
Citizenship: United States of America
Residence: San Leandro, California CA
P.O. Address: 14244 Santiago Road
San Leandro, California 94577

8-00
Eighth Joint Inventor:

Full name: Bao Tran
Signature: _____
Date: _____, 2001
Citizenship: United States of America
Residence: Santa Clara, California CA
P.O. Address: 750 Salberg Avenue
Santa Clara, California 95051

Docket No.: PF-0662 USN

9-80

Ninth Joint Inventor: Full name: Leo L. Shih
 Signature: _____
 Date: _____, 2001
 Citizenship: United States of America
 Residence: East Palo Alto, California CA
 P.O. Address: 908 O'Connor St.
East Palo Alto, California 94303

10-00

Tenth Joint Inventor: Full name: Janice Au-Young
 Signature: Janice Au-Young
 Date: September 7, 2001
 Citizenship: United States of America
 Residence: Brisbane, California CA
 P.O. Address: 233 Golden Eagle Lane
Brisbane, California 94005

Docket No.: PF-0662 USN

**DECLARATION AND POWER OF ATTORNEY FOR
UNITED STATES PATENT APPLICATION**

As a below named inventor, I hereby declare that:

My residence, post office address and citizenship are as stated below next to my name, and

I believe that I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if more than one name is listed below) of the subject matter which is claimed and for which a United States patent is sought on the invention entitled

NUCLEIC-ACID BINDING PROTEINS

the specification of which:

 / is attached hereto.

 / was filed on _____ as application Serial No. _____ and if this box contains an X /, was amended on _____.

 X / was filed as Patent Cooperation Treaty international application No. PCT/US00/02237 on January 28, 2000, this box contains an X /, was amended on under Patent Cooperation Treaty Article 19 on _____ 2001, and if this box contains an X /, was amended on _____.

I hereby state that I have reviewed and understand the contents of the above-identified specification, including the claims, as amended by any amendment referred to above.

I acknowledge my duty to disclose information which is material to the examination of this application in accordance with Title 37, Code of Federal Regulations, §1.56(a).

I hereby claim the benefit under Title 35, United States Code, §119 or §365(a)-(b) of any foreign application(s) for patent or inventor's certificate indicated below and of any Patent Cooperation Treaty international applications(s) designating at least one country other than the United States indicated below and have also identified below any foreign application(s) for patent or inventor's certificate and Patent Cooperation Treaty international application(s) designating at least one country other than the United States for the same subject matter and having a filing date before that of the application for said subject matter the priority of which is claimed:

Docket No.: PF-0662 USN

Country	Number	Filing Date	Priority Claimed
_____	_____	_____	// Yes // No
_____	_____	_____	// Yes // No

I hereby claim the benefit under Title 35, United States Code, §119(e) of any United States provisional application(s) listed below.

Application Serial No.	Filed	Status (Pending, Abandoned, Patented)
60/117,905	January 29, 1999	Expired
60/117,904	January 29, 1999	Expired

I hereby claim the benefit under Title 35, United States Code, §120 of any United States application(s) listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in said prior application(s) in the manner required by the first paragraph of Title 35, United States Code §112, I acknowledge my duty to disclose material information as defined in Title 37 Code of Federal Regulations, §1.56(a) which occurred between the filing date(s) of the prior application(s) and the national or Patent Cooperation Treaty international filing date of this application:

Application Serial No.	Filed	Status (Pending, Abandoned, Patented)
_____	_____	_____

I hereby appoint the following:

Lucy J. Billings	Reg. No. 36,749
Michael C. Cerrone	Reg. No. 39,132
Diana Hamlet-Cox	Reg. No. 33,302
Richard C. Ekstrom	Reg. No. 37,027
Barrie D. Greene	Reg. No. 46,740
Lynn E. Murry	Reg. No. 42,918
Shirley A. Recipon	Reg. No. 47,016
Susan K. Sather	Reg. No. 44,316
Michelle M. Stempien	Reg. No. 41,327
David G. Streeter	Reg. No. 43,168

respectively and individually, as my patent attorneys and/or agents, with full power of substitution and revocation, to prosecute this application and to transact all business in the Patent and Trademark Office connected therewith. Please address all communications to:

Docket No.: PF-0662 USN

**LEGAL DEPARTMENT
INCYTE GENOMICS, INC.
3160 PORTER DRIVE, PALO ALTO, CA 94304**

TEL: 650-855-0555 FAX: 650-849-8886 or 650-845-4166

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issuing thereon.

First Joint Inventor:

Full name:	Y. Tom Tang
Signature:	
Date:	, 2001
Citizenship	United States of America
Residence:	San Jose, California
P.O. Address:	4230 Ranwick Court San Jose, California 95118

Second Joint Inventor:

Full name:	Preeti Lal
Signature:	
Date:	, 2001
Citizenship	India
Residence:	Santa Clara, California
P.O. Address:	P.O. Box 5142 Santa Clara, California 95056

Docket No.: PF-0662 USN

Third Joint Inventor:

Full name: Jennifer L. Hillman
Signature: _____
Date: _____, 2001
Citizenship United States of America
Residence: Mountain View, California
P.O. Address: 230 Monroe Drive, #17
Mountain View, California 94040

Fourth Joint Inventor:

Full name: Henry Yue
Signature: _____
Date: _____, 2001
Citizenship United States of America
Residence: Sunnyvale, California
P.O. Address: 826 Lois Avenue
Sunnyvale, California 94087

Fifth Joint Inventor:

Full name: Yalda Azimzai
Signature: _____
Date: _____, 2001
Citizenship United States of America
Residence: Castro Valley, California
P.O. Address: 5518 Boulder Canyon Dr. Castro
Valley, California 94552

Docket No.: PF-0662 USN

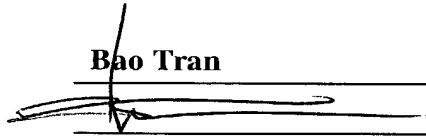
Sixth Joint Inventor:

Full name: Dyung Aina M. Lu
Signature: _____
Date: _____, 2001
Citizenship United States of America
Residence: San Jose, California
P.O. Address: 233 Coy Drive
San Jose, California 95123

Seventh Joint Inventor:

Full name: Mariah R. Baughn
Signature: _____
Date: _____, 2001
Citizenship United States of America
Residence: San Leandro, California
P.O. Address: 14244 Santiago Road
San Leandro, California 94577

Eighth Joint Inventor:

Full name: Bao Tran
Signature: 
Date: Oct 26, 2001
Citizenship United States of America
Residence: Santa Clara, California
P.O. Address: 750 Salberg Avenue
Santa Clara, California 95051

Docket No.: PF-0662 USN

Ninth Joint Inventor:

Full name: Leo L. Shih
Signature: _____
Date: _____, 2001
Citizenship United States of America
Residence: East Palo Alto, California
P.O. Address: 908 O'Connor St.
East Palo Alto, California 94303

Tenth Joint Inventor:

Full name: Janice Au-Young
Signature: _____
Date: _____, 2001
Citizenship United States of America
Residence: Brisbane, California
P.O. Address: 233 Golden Eagle Lane
Brisbane, California 94005

Docket No.: PF-0662 USN

**DECLARATION AND POWER OF ATTORNEY FOR
UNITED STATES PATENT APPLICATION**

As a below named inventor, I hereby declare that:

My residence, post office address and citizenship are as stated below next to my name, and

I believe that I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if more than one name is listed below) of the subject matter which is claimed and for which a United States patent is sought on the invention entitled

NUCLEIC-ACID BINDING PROTEINS

the specification of which:

 / / is attached hereto.

 / / was filed on _____ as application Serial No. _____ and if this box contains an X / / was amended on _____.

 / X / / was filed as Patent Cooperation Treaty international application No. PCT/US00/02237 on January 28, 2000, this box contains an X / /, was amended on under Patent Cooperation Treaty Article 19 on _____ 2001, and if this box contains an X / /, was amended on _____.

I hereby state that I have reviewed and understand the contents of the above-identified specification, including the claims, as amended by any amendment referred to above.

I acknowledge my duty to disclose information which is material to the examination of this application in accordance with Title 37, Code of Federal Regulations, §1.56(a).

I hereby claim the benefit under Title 35, United States Code, §119 or §365(a)-(b) of any foreign application(s) for patent or inventor's certificate indicated below and of any Patent Cooperation Treaty international applications(s) designating at least one country other than the United States indicated below and have also identified below any foreign application(s) for patent or inventor's certificate and Patent Cooperation Treaty international application(s) designating at least one country other than the United States for the same subject matter and having a filing date before that of the application for said subject matter the priority of which is claimed:

Docket No.: PF-0662 USN

Country	Number	Filing Date	Priority Claimed
_____	_____	_____	// Yes // No
_____	_____	_____	// Yes // No

I hereby claim the benefit under Title 35, United States Code, §119(e) of any United States provisional application(s) listed below.

Application	Status (Pending,
Serial No.	Filed
60/117,905	January 29, 1999
60/117,904	January 29, 1999

I hereby claim the benefit under Title 35, United States Code, §120 of any United States application(s) listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in said prior application(s) in the manner required by the first paragraph of Title 35, United States Code §112, I acknowledge my duty to disclose material information as defined in Title 37 Code of Federal Regulations, §1.56(a) which occurred between the filing date(s) of the prior application(s) and the national or Patent Cooperation Treaty international filing date of this application:

Application	Status (Pending,
Serial No.	Filed
_____	_____

I hereby appoint the following:

Lucy J. Billings	Reg. No. 36,749
Michael C. Cerrone	Reg. No. 39,132
Diana Hamlet-Cox	Reg. No. 33,302
Richard C. Ekstrom	Reg. No. 37,027
Barrie D. Greene	Reg. No. 46,740
Lynn E. Murry	Reg. No. 42,918
Shirley A. Recipon	Reg. No. 47,016
Susan K. Sather	Reg. No. 44,316
Michelle M. Stempien	Reg. No. 41,327
David G. Streeter	Reg. No. 43,168
P. Ben Wang	Reg. No. 41,420

respectively and individually, as my patent attorneys and/or agents, with full power of substitution and revocation, to prosecute this application and to transact all business in the Patent and Trademark Office connected therewith. Please address all communications to:

Docket No.: PF-0662 USN

**LEGAL DEPARTMENT
INCYTE GENOMICS, INC.
3160 PORTER DRIVE, PALO ALTO, CA 94304**

TEL: 650-855-0555 FAX: 650-849-8886 or 650-845-4166

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issuing thereon.

First Joint Inventor:	Full name:	Y. Tom Tang
	Signature:	
	Date:	, 2001
	Citizenship	United States of America
	Residence:	San Jose, California
	P.O. Address:	4230 Ranwick Court San Jose, California 95118

Second Joint Inventor:	Full name:	Preeti Lal
	Signature:	
	Date:	, 2001
	Citizenship	India
	Residence:	Santa Clara, California
	P.O. Address:	P.O. Box 5142 Santa Clara, California 95056

Docket No.: PF-0662 USN

Third Joint Inventor:

Full name: Jennifer L. Hillman
Signature: _____
Date: _____, 2001
Citizenship United States of America
Residence: Mountain View, California
P.O. Address: 230 Monroe Drive, #17
Mountain View, California 94040

Fourth Joint Inventor:

Full name: Henry Yue
Signature: _____
Date: _____, 2001
Citizenship United States of America
Residence: Sunnyvale, California
P.O. Address: 826 Lois Avenue
Sunnyvale, California 94087

Fifth Joint Inventor:

Full name: Yalda Azimzai
Signature: _____
Date: _____, 2001
Citizenship United States of America
Residence: Castro Valley, California
P.O. Address: 5518 Boulder Canyon Dr. Castro
Valley, California 94552

Docket No.: PF-0662 USN

Sixth Joint Inventor:

Full name: Dyung Aina M. Lu
Signature: _____
Date: _____, 2001
Citizenship United States of America
Residence: San Jose, California
P.O. Address: 233 Coy Drive
San Jose, California 95123

Seventh Joint Inventor:


Full name: Mariah R. Baughn
Signature: _____
Date: _____, 2001
Citizenship United States of America
Residence: San Leandro, California
P.O. Address: 14244 Santiago Road
San Leandro, California 94577

Eighth Joint Inventor:

Full name: Bao Tran
Signature: _____
Date: _____, 2001
Citizenship United States of America
Residence: Santa Clara, California
P.O. Address: 750 Salberg Avenue
Santa Clara, California 95051

Docket No.: PF-0662 USN

Ninth Joint Inventor:

Full name: Leo L. Shih
Signature: 
Date: October 27, 2001
Citizenship United States of America
Residence: East Palo Alto, California
P.O. Address: 908 O'Connor St.
East Palo Alto, California 94303

Tenth Joint Inventor:

Full name: Janice Au-Young
Signature:
Date: , 2001
Citizenship United States of America
Residence: Brisbane, California
P.O. Address: 233 Golden Eagle Lane
Brisbane, California 94005

SEQUENCE LISTING

<110> INCYTE PHARMACEUTICALS, INC.

TANG, Y. Tom

LAL, Preeti

HILLMAN, Jennifer L.

YUE, Henry

AZIMZAI, Yalda

LU, Aina M.D.

BAUGHN, Mariah R.

TRAN, Bao

SHIH, Leo L.

AU-YOUNG, Janice

<120> NUCLEIC ACID-BINDING PROTEINS

<130> PF-0662 PCT

<140> To Be Assigned

<141> Herewith

<150> 60/117,905; 60/117,904

<151> 1999-01-29; 1999-01-29

<160> 110

<170> PERL Program

<210> 1

<211> 754

<212> PRT

<213> Homo sapiens

<220>

<221> misc-feature

<223> Incyte ID No.: 025733CD1

<400> 1

Met	Ala	Ala	Ala	Gly	Ser	Arg	Lys	Arg	Arg	Leu	Ala	Glu	Leu	Thr
1				5					10					15
Val	Asp	Glu	Phe	Leu	Ala	Ser	Gly	Phe	Asp	Ser	Glu	Ser	Glu	Ser
				20					25					30
Glu	Ser	Glu	Asn	Ser	Pro	Gln	Ala	Glu	Thr	Arg	Glu	Ala	Arg	Glu
				35					40					45
Ala	Ala	Arg	Ser	Pro	Asp	Lys	Pro	Gly	Gly	Ser	Pro	Ser	Ala	Ser
				50					55					60
Arg	Arg	Lys	Gly	Arg	Ala	Ser	Glu	His	Lys	Asp	Gln	Leu	Ser	Arg
				65					70					75
Leu	Lys	Asp	Arg	Asp	Pro	Glu	Phe	Tyr	Lys	Phe	Leu	Gln	Glu	Asn
				80					85					90
Asp	Gln	Ser	Leu	Leu	Asn	Phe	Ser	Asp	Ser	Asp	Ser	Ser	Glu	Glu
				95					100					105
Glu	Glu	Gly	Pro	Phe	His	Ser	Leu	Pro	Asp	Val	Leu	Glu	Glu	Ala
				110					115					120
Ser	Glu	Glu	Glu	Asp	Gly	Ala	Glu	Glu	Gly	Glu	Asp	Gly	Asp	Arg
				125					130					135
Val	Pro	Arg	Gly	Leu	Lys	Gly	Lys	Lys	Asn	Ser	Val	Pro	Val	Thr
				140					145					150
Val	Ala	Met	Val	Glu	Arg	Trp	Lys	Gln	Ala	Ala	Lys	Gln	Arg	Leu
				155					160					165

Thr	Pro	Lys	Leu	Phe	His	Glu	Val	Val	Gln	Ala	Phe	Arg	Ala	Ala	
				170					175					180	
Val	Ala	Thr	Thr	Arg	Gly	Asp	Gln	Glu	Ser	Ala	Glu	Ala	Asn	Lys	
				185					190					195	
Phe	Gln	Val	Thr	Asp	Ser	Ala	Ala	Phe	Asn	Ala	Leu	Val	Thr	Phe	
				200					205					210	
Cys	Ile	Arg	Asp	Leu	Ile	Gly	Cys	Leu	Gln	Lys	Leu	Leu	Phe	Gly	
				215					220					225	
Lys	Val	Ala	Lys	Asp	Ser	Ser	Arg	Met	Leu	Gln	Pro	Ser	Ser	Ser	
				230					235					240	
Pro	Leu	Trp	Gly	Lys	Leu	Arg	Val	Asp	Ile	Lys	Ala	Tyr	Leu	Gly	
				245					250					255	
Ser	Ala	Ile	Gln	Leu	Val	Ser	Cys	Leu	Ser	Glu	Thr	Thr	Val	Leu	
				260					265					270	
Ala	Ala	Val	Leu	Arg	His	Ile	Ser	Val	Leu	Val	Pro	Cys	Phe	Leu	
				275					280					285	
Thr	Phe	Pro	Lys	Gln	Cys	Arg	Met	Leu	Leu	Lys	Arg	Met	Val	Val	
				290					295					300	
Val	Trp	Ser	Thr	Gly	Glu	Glu	Ser	Leu	Arg	Val	Leu	Ala	Phe	Leu	
				305					310					315	
Val	Leu	Ser	Arg	Val	Cys	Arg	His	Lys	Lys	Asp	Thr	Phe	Leu	Gly	
				320					325					330	
Pro	Val	Leu	Lys	Gln	Met	Tyr	Ile	Thr	Tyr	Val	Arg	Asn	Cys	Lys	
				335					340					345	
Phe	Thr	Ser	Pro	Gly	Ala	Leu	Pro	Phe	Ile	Ser	Phe	Met	Gln	Trp	
				350					355					360	
Thr	Leu	Thr	Glu	Leu	Leu	Ala	Leu	Glu	Pro	Gly	Val	Ala	Tyr	Gln	
				365					370					375	
His	Ala	Phe	Leu	Tyr	Ile	Arg	Gln	Leu	Ala	Ile	His	Leu	Arg	Asn	
				380					385					390	
Ala	Met	Thr	Thr	Arg	Lys	Lys	Glu	Thr	Tyr	Gln	Ser	Val	Tyr	Asn	
				395					400					405	
Trp	Gln	Tyr	Val	His	Cys	Leu	Phe	Leu	Trp	Cys	Arg	Val	Leu	Ser	
				410					415					420	
Thr	Ala	Gly	Pro	Ser	Glu	Ala	Leu	Gln	Pro	Leu	Val	Tyr	Pro	Leu	
				425					430					435	
Ala	Gln	Val	Ile	Ile	Gly	Cys	Ile	Lys	Leu	Ile	Pro	Thr	Ala	Arg	
				440					445					450	
Phe	Tyr	Pro	Leu	Arg	Met	His	Cys	Ile	Arg	Ala	Leu	Thr	Leu	Leu	
				455					460					465	
Ser	Gly	Ser	Ser	Gly	Ala	Phe	Ile	Pro	Val	Leu	Pro	Phe	Ile	Leu	
				470					475					480	
Glu	Met	Phe	Gln	Gln	Val	Asp	Phe	Asn	Arg	Lys	Pro	Gly	Arg	Met	
				485					490					495	
Ser	Ser	Lys	Pro	Ile	Asn	Phe	Ser	Val	Ile	Leu	Lys	Leu	Ser	Asn	
				500					505					510	
Val	Asn	Leu	Gln	Glu	Lys	Ala	Tyr	Arg	Asp	Gly	Leu	Val	Glu	Gln	
				515					520					525	
Leu	Tyr	Asp	Leu	Thr	Leu	Glu	Tyr	Leu	His	Ser	Gln	Ala	His	Cys	
				530					535					540	
Ile	Gly	Phe	Pro	Glu	Leu	Val	Leu	Pro	Val	Val	Leu	Gln	Leu	Lys	
				545					550					555	
Ser	Phe	Leu	Arg	Glu	Cys	Lys	Val	Ala	Asn	Tyr	Cys	Arg	Gln	Val	
				560					565					570	
Gln	Gln	Leu	Leu	Gly	Lys	Val	Gln	Glu	Asn	Ser	Ala	Tyr	Ile	Cys	
				575					580					585	
Ser	Arg	Arg	Gln	Arg	Val	Ser	Phe	Gly	Val	Ser	Glu	Gln	Gln	Ala	
				590					595					600	
Val	Glu	Ala	Trp	Glu	Lys	Leu	Thr	Arg	Glu	Glu	Gly	Thr	Pro	Leu	
				605					610					615	

```

Thr Leu Tyr Tyr Ser His Trp Arg Lys Leu Arg Asp Arg Glu Ile
620 625 630
Gln Leu Glu Ile Ser Gly Lys Glu Arg Leu Glu Asp Leu Asn Phe
635 640 645
Pro Glu Ile Lys Arg Arg Lys Met Ala Asp Arg Lys Asp Glu Asp
650 655 660
Arg Lys Gln Phe Lys Asp Leu Phe Asp Leu Asn Ser Ser Glu Glu
665 670 675
Asp Asp Thr Glu Gly Phe Ser Glu Arg Gly Ile Leu Arg Pro Leu
680 685 690
Ser Thr Arg His Gly Val Glu Asp Asp Glu Glu Asp Glu Glu Glu
695 700 705
Gly Glu Glu Asp Ser Ser Asn Ser Glu Gly Glu Trp Ser Trp Asp
710 715 720
Gly Asp Pro Asp Ala Glu Ala Gly Leu Ala Pro Gly Glu Leu Gln
725 730 735
Gln Leu Ala Gln Gly Pro Glu Asp Glu Leu Glu Asp Leu Gln Leu
740 745 750
Ser Glu Asp Asp

```

<210> 2

<211> 593

<212> PRT

<213> Homo sapiens

<220>

<221> misc-feature

<223> Incyte ID No.: 079702CD1

<400> 2

```

Met Arg Asp Ser Thr Gly Ala Gly Asn Ser Leu Val His Lys Arg
1 5 10 15
Ser Pro Leu Arg Arg Asn Gln Lys Thr Pro Thr Ser Leu Thr Lys
20 25 30
Leu Ser Leu Gln Asp Gly His Lys Ala Lys Lys Pro Ala Cys Lys
35 40 45
Phe Glu Glu Gly Gln Asp Val Leu Ala Arg Trp Ser Asp Gly Leu
50 55 60
Phe Tyr Leu Gly Thr Ile Lys Lys Ile Asn Ile Leu Lys Gln Ser
65 70 75
Cys Phe Ile Ile Phe Glu Asp Ser Ser Lys Ser Trp Val Leu Trp
80 85 90
Lys Asp Ile Gln Thr Gly Ala Thr Gly Ser Gly Glu Met Val Cys
95 100 105
Thr Ile Cys Gln Glu Glu Tyr Ser Glu Ala Pro Asn Glu Met Val
110 115 120
Ile Cys Asp Lys Cys Gly Gln Gly Tyr His Gln Leu Cys His Thr
125 130 135
Pro His Ile Asp Ser Ser Val Ile Asp Ser Asp Glu Lys Trp Leu
140 145 150
Cys Arg Gln Cys Val Phe Ala Thr Thr Thr Lys Arg Gly Gly Ala
155 160 165
Leu Lys Lys Gly Pro Asn Ala Lys Ala Leu Gln Val Met Lys Gln
170 175 180
Thr Leu Pro Tyr Ser Val Ala Asp Leu Glu Trp Asp Ala Gly His
185 190 195
Lys Thr Asn Val Gln Gln Cys Tyr Cys Tyr Cys Gly Gly Pro Gly
200 205 210
Asp Trp Tyr Leu Lys Met Leu Gln Cys Cys Lys Cys Lys Gln Trp

```

Phe His Glu Ala	215	Cys Val Gln Cys Leu	220	Gln Lys Pro Met Leu	225	Phe
Gly Asp Arg Phe	230	Tyr Thr Phe Ile Cys	235	Ser Val Cys Ser Ser	240	Gly
Pro Glu Tyr Leu	245	Lys Arg Leu Pro Leu	250	Gln Trp Val Asp Ile	255	Ala
His Leu Cys Leu	260	Tyr Asn Leu Ser Val	265	Ile His Lys Lys Lys	270	Tyr
Phe Asp Ser Glu	275	Leu Glu Leu Met Thr	280	Tyr Ile Asn Glu Asn	285	Trp
Asp Arg Leu His	290	Pro Gly Glu Leu Ala	295	Asp Thr Pro Lys Ser	300	Glu
Arg Tyr Glu His	305	Val Leu Glu Ala Leu	310	Asn Asp Tyr Lys Thr	315	Met
Phe Met Ser Gly	320	Lys Glu Ile Lys Lys	325	Lys Lys His Leu Phe	330	Gly
	335		340		345	
Leu Arg Ile Arg	350	Val Pro Pro Val Pro	355	Pro Asn Val Ala Phe	360	Lys
Ala Glu Lys Glu	365	Pro Glu Gly Thr Ser	370	His Glu Phe Lys Ile	375	Lys
Gly Arg Lys Ala	380	Ser Lys Pro Ile Ser	385	Asp Ser Arg Glu Val	390	Ser
Asn Gly Ile Glu	395	Lys Lys Lys Lys Lys	400	Lys Ser Val Gly Arg	405	Pro
Pro Gly Pro Tyr	410	Thr Arg Lys Met Ile	415	Gln Lys Thr Ala Glu	420	Pro
Leu Leu Asp Lys	425	Glu Ser Ile Ser Glu	430	Asn Pro Thr Leu Asp	435	Leu
Pro Cys Ser Ile	440	Gly Arg Thr Glu Gly	445	Thr Ala His Ser Ser	450	Asn
Thr Ser Asp Val	455	Asp Phe Thr Gly Ala	460	Ser Ser Ala Lys Glu	465	Thr
Thr Ser Ser Ser	470	Ile Ser Arg His Tyr	475	Gly Leu Ser Asp Ser	480	Arg
Lys Arg Thr Arg	485	Thr Gly Arg Ser Trp	490	Pro Ala Ala Ile Pro	495	His
Leu Arg Arg Arg	500	Arg Gly Arg Leu Pro	505	Arg Arg Ala Leu Gln	510	Thr
Gln Asn Ser Glu	515	Ile Val Lys Asp Asp	520	Glu Gly Lys Glu Asp	525	Tyr
Gln Phe Asp Glu	530	Leu Asn Thr Glu Ile	535	Leu Asn Asn Leu Ala	540	Asp
Gln Glu Leu Gln	545	Leu Asn His Leu Lys	550	Asn Ser Ile Thr Ser	555	Tyr
Phe Gly Ala Ala	560	Gly Arg Ile Ala Cys	565	Gly Glu Lys Tyr Arg	570	Val
Leu Ala Arg Arg	575	Val Thr Leu Asp Gly	580	Lys Val Gln Tyr Leu	585	Val
Glu Trp Glu Gly	590	Ala Thr Ala Ser				

<210> 3
 <211> 534
 <212> PRT
 <213> Homo sapiens
 <220>

<221> misc-feature

<223> Incyte ID No.: 116208CD1

<400> 3

Met	Arg	Ala	Leu	His	Leu	Leu	Lys	Ser	Gly	Cys	Ser	Pro	Ala	Val	
1				5					10					15	
Gln	Ile	Lys	Ile	Arg	Glu	Leu	Tyr	Arg	Arg	Arg	Tyr	Pro	Arg	Thr	
				20					25					30	
Leu	Glu	Gly	Leu	Ser	Asp	Leu	Ser	Thr	Ile	Lys	Ser	Ser	Val	Phe	
				35					40					45	
Ser	Leu	Asp	Gly	Gly	Ser	Ser	Pro	Val	Glu	Pro	Asp	Leu	Ala	Val	
				50					55					60	
Ala	Gly	Ile	His	Ser	Leu	Pro	Ser	Thr	Ser	Val	Thr	Pro	His	Ser	
				65					70					75	
Pro	Ser	Ser	Pro	Val	Gly	Ser	Val	Leu	Leu	Gln	Asp	Thr	Lys	Pro	
				80					85					90	
Thr	Phe	Glu	Met	Gln	Gln	Pro	Ser	Pro	Pro	Ile	Pro	Pro	Val	His	
				95					100					105	
Pro	Asp	Val	Gln	Leu	Lys	Asn	Leu	Pro	Phe	Tyr	Asp	Val	Leu	Asp	
				110					115					120	
Val	Leu	Ile	Lys	Pro	Thr	Ser	Leu	Val	Gln	Ser	Ser	Ile	Gln	Arg	
				125					130					135	
Phe	Gln	Glu	Lys	Phe	Phe	Ile	Phe	Ala	Leu	Thr	Pro	Gln	Gln	Val	
				140					145					150	
Arg	Glu	Ile	Cys	Ile	Ser	Arg	Asp	Phe	Leu	Pro	Gly	Gly	Arg	Arg	
				155					160					165	
Asp	Tyr	Thr	Val	Gln	Val	Gln	Leu	Arg	Leu	Cys	Leu	Ala	Glu	Thr	
				170					175					180	
Ser	Cys	Pro	Gln	Glu	Asp	Asn	Tyr	Pro	Asn	Ser	Leu	Cys	Ile	Lys	
				185					190					195	
Val	Asn	Gly	Lys	Leu	Phe	Pro	Leu	Pro	Gly	Tyr	Ala	Pro	Pro	Pro	
				200					205					210	
Lys	Asn	Gly	Ile	Glu	Gln	Lys	Arg	Pro	Gly	Arg	Pro	Leu	Asn	Ile	
				215					220					225	
Thr	Ser	Leu	Val	Arg	Leu	Ser	Ser	Ala	Val	Pro	Asn	Gln	Ile	Ser	
				230					235					240	
Ile	Ser	Trp	Ala	Ser	Glu	Ile	Gly	Lys	Asn	Tyr	Ser	Met	Ser	Val	
				245					250					255	
Tyr	Leu	Val	Arg	Gln	Leu	Thr	Ser	Ala	Met	Leu	Leu	Gln	Arg	Leu	
				260					265					270	
Lys	Met	Lys	Gly	Ile	Arg	Asn	Pro	Asp	His	Ser	Arg	Ala	Leu	Ser	
				275					280					285	
Lys	Glu	Lys	Leu	Thr	Ala	Asp	Pro	Asp	Ser	Glu	Ile	Ala	Thr	Thr	
				290					295					300	
Ser	Leu	Arg	Val	Ser	Leu	Met	Cys	Pro	Leu	Gly	Lys	Met	Arg	Leu	
				305					310					315	
Thr	Ile	Pro	Cys	Arg	Ala	Val	Thr	Cys	Thr	His	Leu	Gln	Cys	Phe	
				320					325					330	
Asp	Ala	Ala	Leu	Tyr	Leu	Gln	Met	Asn	Glu	Lys	Lys	Pro	Thr	Trp	
				335					340					345	
Ile	Cys	Pro	Val	Cys	Asp	Lys	Lys	Ala	Ala	Tyr	Glu	Ser	Leu	Ile	
				350					355					360	
Leu	Asp	Gly	Leu	Phe	Met	Glu	Ile	Leu	Asn	Asp	Cys	Ser	Asp	Val	
				365					370					375	
Asp	Glu	Ile	Lys	Phe	Gln	Glu	Asp	Gly	Ser	Trp	Cys	Pro	Met	Arg	
				380					385					390	
Pro	Lys	Lys	Glu	Ala	Met	Lys	Val	Ser	Ser	Gln	Pro	Cys	Thr	Lys	
				395					400					405	
Ile	Glu	Ser	Ser	Ser	Val	Leu	Ser	Lys	Pro	Cys	Ser	Val	Thr	Val	
				410					415					420	
Ala	Ser	Glu	Ala	Ser	Lys	Lys	Lys	Val	Asp	Val	Ile	Asp	Leu	Thr	
				425					430					435	

```

Ile Glu Ser Ser Ser Asp Glu Glu Glu Asp Pro Pro Ala Lys Arg
      440      445      450
Lys Cys Ile Phe Met Ser Glu Thr Gln Ser Ser Pro Thr Lys Gly
      455      460      465
Val Leu Met Tyr Gln Pro Ser Ser Val Arg Val Pro Ser Val Thr
      470      475      480
Ser Val Asp Pro Ala Ala Ile Pro Pro Ser Leu Thr Asp Tyr Ser
      485      490      495
Val Pro Phe His His Thr Pro Ile Ser Ser Met Ser Ser Asp Leu
      500      505      510
Pro Gly Glu Gln Arg Arg Asn Asp Ile Asn Asn Glu Leu Lys Leu
      515      520      525
Gly Thr Ser Ser Asp Thr Val Gln Gln
      530

```

```

<210> 4
<211> 255
<212> PRT
<213> Homo sapiens

<220>
<221> misc feature
<223> Incyte ID No.: 179261CD1

```

```

<400> 4
Met Lys Ile Ile Ser Glu Asn Val Pro Ser Tyr Lys Thr His Glu
 1      5      10      15
Ser Leu Thr Leu Pro Arg Arg Thr His Asp Ser Glu Lys Pro Tyr
      20      25      30
Glu Tyr Lys Glu Tyr Glu Lys Val Phe Ser Cys Asp Leu Glu Phe
      35      40      45
Asp Glu Tyr Gln Lys Ile His Thr Gly Gly Lys Asn Tyr Glu Cys
      50      55      60
Asn Gln Cys Trp Lys Thr Phe Gly Ile Asp Asn Ser Ser Met Leu
      65      70      75
Gln Leu Asn Ile His Thr Gly Val Lys Pro Cys Lys Tyr Met Glu
      80      85      90
Tyr Gly Asn Thr Cys Ser Phe Tyr Lys Asp Phe Asn Val Tyr Gln
      95      100      105
Lys Ile His Asn Glu Lys Phe Tyr Lys Cys Lys Glu Tyr Arg Arg
      110      115      120
Thr Phe Glu Arg Val Gly Lys Val Thr Pro Leu Gln Arg Val His
      125      130      135
Asp Gly Glu Lys His Phe Glu Cys Ser Phe Cys Gly Lys Ser Phe
      140      145      150
Arg Val His Ala Gln Leu Thr Arg His Gln Lys Ile His Thr Asp
      155      160      165
Glu Lys Thr Tyr Lys Cys Met Glu Cys Gly Lys Asp Phe Arg Phe
      170      175      180
His Ser Gln Leu Thr Glu His Gln Arg Ile His Thr Gly Glu Lys
      185      190      195
Pro Tyr Lys Cys Met His Cys Glu Lys Val Phe Arg Ile Ser Ser
      200      205      210
Gln Leu Ile Glu His Gln Arg Ile His Thr Gly Glu Lys Pro Tyr
      215      220      225
Ala Cys Lys Glu Cys Gly Lys Ala Phe Gly Val Cys Arg Glu Leu
      230      235      240
Ala Arg His Gln Arg Ile His Thr Gly Lys Tyr Cys Gly Trp Ile
      245      250      255

```

<210> 5
 <211> 562
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc feature
 <223> Incyte ID No.: 259161CD1

<400> 5

Met	Ala	Ser	Val	Ser	Ala	Leu	Thr	Glu	Glu	Leu	Asp	Ser	Ile	Thr
1				5					10					15
Ser	Glu	Leu	His	Ala	Val	Glu	Ile	Gln	Ile	Gln	Glu	Leu	Thr	Glu
				20					25					30
Arg	Gln	Gln	Glu	Leu	Ile	Gln	Lys	Lys	Lys	Val	Leu	Thr	Lys	Lys
				35					40					45
Ile	Lys	Gln	Cys	Leu	Glu	Asp	Ser	Asp	Ala	Gly	Ala	Ser	Asn	Glu
				50					55					60
Tyr	Asp	Ser	Ser	Pro	Ala	Ala	Trp	Asn	Lys	Glu	Asp	Phe	Pro	Trp
				65					70					75
Ser	Gly	Lys	Val	Lys	Asp	Ile	Leu	Gln	Asn	Val	Phe	Lys	Leu	Glu
				80					85					90
Lys	Phe	Arg	Pro	Leu	Gln	Leu	Glu	Thr	Ile	Asn	Val	Thr	Met	Ala
				95					100					105
Gly	Lys	Glu	Val	Phe	Leu	Val	Met	Pro	Thr	Gly	Gly	Gly	Lys	Ser
				110					115					120
Leu	Cys	Tyr	Gln	Leu	Pro	Ala	Leu	Cys	Ser	Asp	Gly	Phe	Thr	Leu
				125					130					135
Val	Ile	Cys	Pro	Leu	Ile	Ser	Leu	Met	Glu	Asp	Gln	Leu	Met	Val
				140					145					150
Leu	Lys	Gln	Leu	Gly	Ile	Ser	Ala	Thr	Met	Leu	Asn	Ala	Ser	Ser
				155					160					165
Ser	Lys	Glu	His	Val	Lys	Trp	Val	His	Ala	Glu	Met	Val	Asn	Lys
				170					175					180
Asn	Ser	Glu	Leu	Lys	Leu	Ile	Tyr	Val	Thr	Pro	Glu	Lys	Ile	Ala
				185					190					195
Lys	Ser	Lys	Met	Phe	Met	Ser	Arg	Leu	Glu	Lys	Ala	Tyr	Glu	Ala
				200					205					210
Arg	Arg	Phe	Thr	Arg	Ile	Ala	Val	Asp	Glu	Val	His	Cys	Cys	Ser
				215					220					225
Gln	Trp	Gly	His	Asp	Phe	Arg	Pro	Asp	Tyr	Lys	Ala	Leu	Gly	Ile
				230					235					240
Leu	Lys	Arg	Gln	Phe	Pro	Asn	Ala	Ser	Leu	Ile	Gly	Leu	Thr	Ala
				245					250					255
Thr	Ala	Thr	Asn	His	Val	Leu	Thr	Asp	Ala	Gln	Lys	Ile	Leu	Cys
				260					265					270
Ile	Glu	Lys	Cys	Phe	Thr	Phe	Thr	Ala	Ser	Phe	Asn	Lys	Pro	Asp
				275					280					285
Val	Arg	Phe	Val	Ile	His	His	Ser	Met	Ser	Lys	Ser	Met	Glu	Asn
				290					295					300
Tyr	Tyr	Gln	Glu	Ser	Gly	Arg	Ala	Gly	Arg	Asp	Asp	Met	Lys	Ala
				305					310					315
Asp	Cys	Ile	Leu	Tyr	Tyr	Gly	Phe	Gly	Asp	Ile	Phe	Arg	Ile	Ser
				320					325					330
Ser	Met	Val	Val	Met	Glu	Asn	Val	Gly	Gln	Gln	Lys	Leu	Tyr	Glu
				335					340					345
Met	Val	Ser	Tyr	Cys	Gln	Asn	Ile	Ser	Lys	Cys	Arg	Arg	Val	Leu
				350					355					360
Met	Ala	Gln	His	Phe	Asp	Glu	Val	Trp	Asn	Ser	Glu	Ala	Cys	Asn

Lys Met Cys Asp	365	Asn Cys Cys Lys Asp	370	Ser Ala Phe Glu Arg Lys	375
Asn Ile Thr Glu	380	Tyr Cys Arg Asp Leu	385	Ile Lys Ile Leu Lys Gln	390
Ala Glu Glu Leu	395	Asn Glu Lys Leu Thr	400	Pro Leu Lys Leu Ile Asp	405
Ser Trp Met Gly	410	Lys Gly Ala Ala Lys	415	Leu Arg Val Ala Gly Val	420
Val Ala Pro Thr	425	Leu Pro Arg Glu Asp	430	Leu Glu Lys Ile Ile Ala	435
His Phe Leu Ile	440	Gln Gln Tyr Leu Lys	445	Glu Asp Tyr Ser Phe Thr	450
Ala Tyr Ala Thr	455	Ile Ser Tyr Leu Lys	460	Gly Pro Lys Ala Asn	465
Leu Leu Asn Asn	470	Glu Ala His Ala Ile	475	Thr Met Gln Val Thr Lys	480
Ser Thr Gln Asn	485	Ser Phe Arg Ala Glu	490	Ser Ser Gln Thr Cys His	495
Ser Glu Gln Gly	500	Asp Lys Lys Ile Gly	505	Gly Lys Lys Phe Gln Ala	510
Thr Ser Arg Arg	515	Arg Leu Gln Thr Cys	520	Phe Ser Asn Leu Val Leu	525
Arg Ile Gln Glu	530	Leu Arg Lys Glu Lys	535	Ser Met Met Pro Asp Met	540
Thr Val Thr Lys	545	Phe Ser Asn	550		555
	560				

<210> 6

<211> 432

<212> PRT

<213> Homo sapiens

<220>

<221> misc-feature

<223> Incyte ID No.: 320087CD1

<400> 6

Met Ser Glu Leu Lys	5	Asp Cys Pro Leu Gln	10	Phe His Asp Phe Lys	15
Ser Val Asp His Leu	20	Lys Val Cys Pro Arg	25	Tyr Thr Ala Val Leu	30
Ala Arg Ser Glu Asp	35	Asp Gly Ile Gly Ile	40	Glu Glu Leu Asp Thr	45
Leu Gln Leu Glu Leu	50	Glu Thr Leu Leu Ser	55	Ser Ala Ser Arg Arg	60
Leu Arg Val Leu Glu	65	Ala Glu Thr Gln Ile	70	Leu Thr Asp Trp Gln	75
Asp Lys Lys Gly Asp	80	Arg Arg Phe Leu Lys	85	Leu Gly Arg Asp His	90
Glu Leu Gly Ala Pro	95	Pro Lys His Gly Lys	100	Pro Lys Lys Gln Lys	105
Leu Glu Gly Lys Ala	110	Gly His Gly Pro Gly	115	Pro Gly Pro Gly Arg	120
Pro Lys Ser Lys Asn	125	Leu Gln Pro Lys Ile	130	Gln Glu Tyr Glu Phe	135
Thr Asp Asp Pro Ile	140	Asp Val Pro Arg Ile	145	Pro Lys Asn Asp Ala	150


```

Pro Asn Arg Phe Trp Ala Ser Val Glu Pro Tyr Cys Ala Asp Ile
155 160 165
Thr Ser Glu Glu Val Arg Thr Leu Glu Glu Leu Leu Lys Pro Pro
170 175 180
Glu Asp Glu Ala Glu His Tyr Lys Ile Pro Pro Leu Gly Lys His
185 190 195
Tyr Ser Gln Arg Trp Ala Gln Glu Asp Leu Leu Glu Glu Gln Lys
200 205 210
Asp Gly Ala Arg Ala Ala Ala Val Ala Asp Lys Lys Lys Gly Leu
215 220 225
Met Gly Pro Leu Thr Glu Leu Asp Thr Lys Asp Val Asp Ala Leu
230 235 240
Leu Lys Lys Ser Glu Ala Gln His Glu Gln Pro Glu Asp Gly Cys
245 250 255
Pro Phe Gly Ala Leu Thr Gln Arg Leu Leu Gln Ala Leu Val Glu
260 265 270
Glu Asn Ile Ile Ser Pro Met Glu Asp Ser Pro Ile Pro Asp Met
275 280 285
Ser Gly Lys Glu Ser Gly Ala Asp Gly Ala Ser Thr Ser Pro Arg
290 295 300
Asn Gln Asn Lys Pro Phe Ser Val Pro His Thr Lys Ser Leu Glu
305 310 315
Ser Arg Ile Lys Glu Glu Leu Ile Ala Gln Gly Leu Leu Glu Ser
320 325 330
Glu Asp Arg Pro Ala Glu Asp Ser Glu Asp Glu Val Leu Ala Glu
335 340 345
Leu Arg Lys Arg Gln Ala Glu Leu Lys Ala Leu Ser Ala His Asn
350 355 360
Arg Thr Lys Lys His Asp Leu Leu Arg Leu Ala Lys Glu Glu Val
365 370 375
Ser Arg Gln Glu Leu Arg Gln Arg Val Arg Met Ala Asp Asn Glu
380 385 390
Val Met Asp Ala Phe Arg Lys Ile Met Ala Ala Arg Gln Lys Lys
395 400 405
Arg Thr Pro Thr Lys Lys Glu Lys Asp Gln Ala Trp Lys Thr Leu
410 415 420
Lys Glu Arg Glu Ser Ile Leu Lys Leu Leu Asp Gly
425 430

```

<210> 7
 <211> 799
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc-feature
 <223> 491271CD1

```

<400> 7
Met Pro Ser Gln Asn Tyr Asp Leu Pro Gln Lys Lys Gln Glu Lys
1 5 10 15
Met Thr Lys Phe Gln Glu Ala Val Thr Phe Lys Asp Val Ala Val
20 25 30
Val Phe Ser Arg Glu Glu Leu Arg Leu Leu Asp Leu Thr Gln Arg
35 40 45
Lys Leu Tyr Arg Asp Val Met Val Glu Asn Phe Lys Asn Leu Val
50 55 60
Ala Val Gly His Leu Pro Phe Gln Pro Asp Met Val Ser Gln Leu
65 70 75

```

WO 00/44900

PCT/US00/02237

Glu	Ala	Glu	Glu	Lys	Leu	Trp	Met	Met	Glu	Thr	Glu	Thr	Gln	Arg
				80					85					90
Ser	Ser	Lys	His	Gln	Asn	Lys	Met	Glu	Thr	Leu	Gln	Lys	Phe	Ala
				95					100					105
Leu	Lys	Tyr	Leu	Ser	Asn	Gln	Glu	Leu	Ser	Cys	Trp	Gln	Ile	Trp
				110					115					120
Lys	Gln	Val	Ala	Ser	Glu	Leu	Thr	Arg	Cys	Leu	Gln	Gly	Lys	Ser
				125					130					135
Ser	Gln	Leu	Leu	Gln	Gly	Asp	Ser	Ile	Gln	Val	Ser	Glu	Asn	Glu
				140					145					150
Asn	Asn	Ile	Met	Asn	Pro	Lys	Gly	Asp	Ser	Pro	Ile	Tyr	Ile	Glu
				155					160					165
Asn	Gln	Glu	Phe	Pro	Phe	Trp	Arg	Thr	Gln	His	Ser	Cys	Gly	Asn
				170					175					180
Thr	Tyr	Leu	Ser	Glu	Ser	Gln	Ile	Gln	Ser	Arg	Gly	Lys	Gln	Ile
				185					190					195
Asp	Val	Lys	Asn	Asn	Leu	Gln	Ile	Arg	Glu	Asp	Phe	Val	Lys	Lys
				200					205					210
Ser	Pro	Phe	His	Glu	His	Ile	Lys	Thr	Asp	Thr	Glu	Pro	Lys	Pro
				215					220					225
Cys	Lys	Gly	Asn	Glu	Tyr	Gly	Lys	Ile	Ile	Ser	Asp	Gly	Ser	Asn
				230					235					240
Gln	Lys	Leu	Pro	Leu	Gly	Glu	Lys	Pro	His	Pro	Cys	Gly	Glu	Cys
				245					250					255
Gly	Arg	Gly	Phe	Ser	Tyr	Ser	Pro	Arg	Leu	Pro	Leu	His	Pro	Asn
				260					265					270
Val	His	Thr	Gly	Glu	Lys	Cys	Phe	Ser	Gln	Ser	Ser	His	Leu	Arg
				275					280					285
Thr	His	Gln	Arg	Ile	His	Pro	Gly	Glu	Lys	Leu	Asn	Arg	Cys	His
				290					295					300
Glu	Ser	Gly	Asp	Cys	Phe	Asn	Lys	Ser	Ser	Phe	His	Ser	Tyr	Gln
				305					310					315
Ser	Asn	His	Thr	Gly	Glu	Lys	Ser	Tyr	Arg	Cys	Asp	Ser	Cys	Gly
				320					325					330
Lys	Gly	Phe	Ser	Ser	Ser	Thr	Gly	Leu	Ile	Ile	His	Tyr	Arg	Thr
				335					340					345
His	Thr	Gly	Glu	Lys	Pro	Tyr	Lys	Cys	Glu	Glu	Cys	Gly	Lys	Cys
				350					355					360
Phe	Ser	Gln	Ser	Ser	Asn	Phe	Gln	Cys	His	Gln	Arg	Val	His	Thr
				365					370					375
Glu	Glu	Lys	Pro	Tyr	Lys	Cys	Glu	Glu	Cys	Gly	Lys	Gly	Phe	Gly
				380					385					390
Trp	Ser	Val	Asn	Leu	Arg	Val	His	Gln	Arg	Val	His	Arg	Gly	Glu
				395					400					405
Lys	Pro	Tyr	Lys	Cys	Glu	Glu	Cys	Gly	Lys	Gly	Phe	Thr	Gln	Ala
				410					415					420
Ala	His	Phe	His	Ile	His	Gln	Arg	Val	His	Thr	Gly	Glu	Lys	Pro
				425					430					435
Tyr	Lys	Cys	Asp	Val	Cys	Gly	Lys	Gly	Phe	Ser	His	Asn	Ser	Pro
				440					445					450
Leu	Ile	Cys	His	Arg	Arg	Val	His	Thr	Gly	Glu	Lys	Pro	Tyr	Lys
				455					460					465
Cys	Glu	Ala	Cys	Gly	Lys	Gly	Phe	Thr	Arg	Asn	Thr	Asp	Leu	His
				470					475					480
Ile	His	Phe	Arg	Val	His	Thr	Gly	Glu	Lys	Pro	Tyr	Lys	Cys	Lys
				485					490					495
Glu	Cys	Gly	Lys	Gly	Phe	Ser	Gln	Ala	Ser	Asn	Leu	Gln	Val	His
				500					505					510
Gln	Asn	Val	His	Thr	Gly	Glu	Lys	Arg	Phe	Lys	Cys	Glu	Thr	Cys
				515					520					525
Gly	Lys	Gly	Phe	Ser	Gln	Ser	Ser	Lys	Leu	Gln	Thr	His	Gln	Arg

10/91

SUBSTITUTE SHEET (RULE 26)

Val His Thr Gly	530	535	540
Glu Lys Pro Tyr Arg Cys Asp Val Cys Gly Lys			
545	550	555	
Asp Phe Ser Tyr Ser Ser Asn Leu Lys Leu His Gln Val Ile His			
560	565	570	
Thr Gly Glu Lys Pro Tyr Lys Cys Glu Glu Cys Gly Lys Gly Phe			
575	580	585	
Ser Trp Arg Ser Asn Leu His Ala His Gln Arg Val His Ser Gly			
590	595	600	
Glu Lys Pro Tyr Lys Cys Glu Gln Cys Asp Lys Ser Phe Ser Gln			
605	610	615	
Ala Ile Asp Phe Arg Val His Gln Arg Val His Thr Gly Glu Lys			
620	625	630	
Pro Tyr Lys Cys Gly Val Cys Gly Lys Gly Phe Ser Gln Ser Ser			
635	640	645	
Gly Leu Gln Ser His Gln Arg Val His Thr Gly Glu Lys Pro Tyr			
650	655	660	
Lys Cys Asp Val Cys Gly Lys Gly Phe Arg Tyr Ser Ser Gln Phe			
665	670	675	
Ile Tyr His Gln Arg Gly His Thr Gly Glu Lys Pro Tyr Lys Cys			
680	685	690	
Glu Glu Cys Gly Lys Gly Phe Gly Arg Ser Leu Asn Leu Arg His			
695	700	705	
His Gln Arg Val His Thr Gly Glu Lys Pro His Ile Cys Glu Glu			
710	715	720	
Cys Gly Lys Ala Phe Ser Leu Pro Ser Asn Leu Arg Val His Leu			
725	730	735	
Gly Val His Thr Arg Glu Lys Leu Phe Lys Cys Glu Glu Cys Gly			
740	745	750	
Lys Gly Phe Ser Gln Ser Ala Arg Leu Glu Ala His Gln Arg Val			
755	760	765	
His Thr Gly Glu Lys Pro Tyr Lys Cys Asp Ile Cys Asp Lys Asp			
770	775	780	
Phe Arg His Arg Ser Arg Leu Thr Tyr His Gln Lys Val His Thr			
785	790	795	
Gly Lys Lys Leu			

<210> 8

<211> 137

<212> PRT

<213> Homo sapiens

<220>

<221> misc-feature

<223> Incyte ID No.: 585172CD1

<400> 8

Met Leu Ser Gly Arg Leu Val Leu Gly Leu Val Ser Met Ala Gly		
1	5	10
Arg Val Cys Leu Cys Gln Gly Ser Ala Gly Ser Gly Ala Ile Gly		
20	25	30
Pro Val Glu Ala Ala Ile Arg Thr Lys Leu Glu Glu Ala Leu Ser		
35	40	45
Pro Glu Val Leu Glu Leu Arg Asn Glu Ser Gly Gly His Ala Val		
50	55	60
Pro Pro Gly Ser Glu Thr His Phe Arg Val Ala Val Val Ser Ser		
65	70	75
Arg Phe Glu Gly Leu Ser Pro Leu Gln Arg His Arg Leu Val His		

<220>

<221> misc-feature

<223> Incyte ID No.: 997067CD1

<400> 10

```

Met Glu Thr Gln Ala Asp Leu Val Ser Gln Glu Pro Gln Ala Leu
  1          5          10          15
Leu Asp Ser Ala Leu Pro Ser Lys Val Pro Ala Phe Ser Asp Lys
          20          25          30
Asp Ser Leu Gly Asp Glu Met Leu Ala Ala Leu Leu Lys Ala
          35          40          45
Lys Ser Gln Glu Leu Val Thr Phe Glu Asp Val Ala Val Tyr Phe
          50          55          60
Ile Arg Lys Glu Trp Lys Arg Leu Glu Pro Ala Gln Arg Asp Leu
          65          70          75
Tyr Arg Asp Val Met Leu Glu Asn Tyr Gly Asn Val Phe Ser Leu
          80          85          90
Asp Arg Glu Thr Arg Thr Glu Asn Asp Gln Glu Ile Ser Glu Asp
          95          100          105
Thr Arg Ser His Gly Val Leu Leu Gly Arg Phe Gln Lys Asp Ile
          110          115          120
Ser Gln Gly Leu Lys Phe Lys Glu Ala Tyr Glu Arg Glu Val Ser
          125          130          135
Leu Lys Arg Pro Leu Gly Asn Ser Pro Gly Glu Arg Leu Asn Arg
          140          145          150
Lys Met Pro Asp Phe Gly Gln Val Thr Val Glu Glu Lys Leu Thr
          155          160          165
Pro Arg Gly Glu Arg Ser Glu Lys Tyr Asn Asp Phe Gly Asn Ser
          170          175          180
Phe Thr Val Asn Ser Asn Leu Ile Ser His Gln Arg Leu Pro Val
          185          190          195
Gly Asp Arg Pro His Lys Cys Asp Glu Cys Ser Lys Ser Phe Asn
          200          205          210
Arg Thr Ser Asp Leu Ile Gln His Gln Arg Ile His Thr Gly Glu
          215          220          225
Lys Pro Tyr Glu Cys Asn Glu Cys Gly Lys Ala Phe Ser Gln Ser
          230          235          240
Ser His Leu Ile Gln His Gln Arg Ile His Thr Gly Glu Lys Pro
          245          250          255
Tyr Glu Cys Ser Asp Cys Gly Lys Thr Phe Ser Cys Ser Ser Ala
          260          265          270
Leu Ile Leu His Arg Arg Ile His Thr Gly Glu Lys Pro Tyr Glu
          275          280          285
Cys Asn Glu Cys Gly Lys Thr Phe Ser Trp Ser Ser Thr Leu Thr
          290          295          300
His His Gln Arg Ile His Thr Gly Glu Lys Pro Tyr Ala Cys Asn
          305          310          315
Glu Cys Gly Lys Ala Phe Ser Arg Ser Ser Thr Leu Ile His His
          320          325          330
Gln Arg Ile His Thr Gly Glu Lys Pro Tyr Glu Cys Asn Glu Cys
          335          340          345
Gly Lys Ala Phe Ser Gln Ser Ser His Leu Tyr Gln His Gln Arg
          350          355          360
Ile His Thr Gly Glu Lys Pro Tyr Glu Cys Met Glu Cys Gly Gly
          365          370          375
Lys Phe Thr Tyr Ser Ser Gly Leu Ile Gln His Gln Arg Ile His
          380          385          390
Thr Gly Glu Asn Pro Tyr Glu Cys Ser Glu Cys Gly Lys Ala Phe
          395          400          405
Arg Tyr Ser Ser Ala Leu Val Arg His Gln Arg Ile His Thr Gly
          410          415          420
Glu Lys Pro Leu Asn Gly Ile Gly Met Ser Lys Ser Ser Leu Arg

```



```

Leu Asp Cys Ala Met Asp Ala Cys Ile Asn Leu Gly Leu Leu Glu
      335      340      345
Glu Ala Leu Phe Tyr Gly Thr Arg Thr Met Glu Pro Tyr Arg Ile
      350      355      360
Phe Phe Pro Gly Ser His Pro Val Arg Gly Val Gln Val Met Lys
      365      370      375
Val Gly Lys Leu Gln Leu His Gln Gly Met Phe Pro Gln Ala Met
      380      385      390
Lys Asn Leu Arg Leu Ala Phe Asp Ile Met Arg Val Thr His Gly
      395      400      405
Arg Glu His Ser Leu Ile Glu Asp Leu Ile Leu Leu Leu Glu Glu
      410      415      420
Cys Asp Ala Asn Ile Arg Ala Ser
      425

```

<210> 12

<211> 590

<212> PRT

<213> Homo sapiens

<220>

<221> misc-feature

<223> Incyte ID No.: 1521648CD1

<400> 12

```

Met Ala Glu Asp Trp Leu Asp Cys Pro Ala Leu Gly Pro Gly Trp
  1      5      10      15
Lys Arg Arg Glu Val Phe Arg Lys Ser Gly Ala Thr Cys Gly Arg
      20      25      30
Ser Asp Thr Tyr Tyr Gln Ser Pro Thr Gly Asp Arg Ile Arg Ser
      35      40      45
Lys Val Glu Leu Thr Arg Tyr Leu Gly Pro Ala Cys Asp Leu Thr
      50      55      60
Leu Phe Asp Phe Lys Gln Gly Ile Leu Cys Tyr Pro Ala Pro Lys
      65      70      75
Ala His Pro Val Ala Val Ala Ser Lys Lys Arg Lys Lys Pro Ser
      80      85      90
Arg Pro Ala Lys Thr Arg Lys Arg Gln Val Gly Pro Gln Ser Gly
      95      100      105
Glu Val Arg Lys Glu Ala Pro Arg Asp Glu Thr Lys Ala Asp Thr
      110      115      120
Asp Thr Ala Pro Ala Ser Phe Pro Ala Pro Gly Cys Cys Glu Asn
      125      130      135
Cys Gly Ile Ser Phe Ser Gly Asp Gly Thr Gln Arg Gln Arg Leu
      140      145      150
Lys Thr Leu Cys Lys Asp Cys Arg Ala Gln Arg Ile Ala Phe Asn
      155      160      165
Arg Glu Gln Arg Met Phe Lys Arg Val Gly Cys Gly Glu Cys Ala
      170      175      180
Ala Cys Gln Val Thr Glu Asp Cys Gly Ala Cys Ser Thr Cys Leu
      185      190      195
Leu Gln Leu Pro His Asp Val Ala Ser Gly Leu Phe Cys Lys Cys
      200      205      210
Glu Arg Arg Arg Cys Leu Arg Ile Val Glu Arg Ser Arg Gly Cys
      215      220      225
Gly Val Cys Arg Gly Cys Gln Thr Gln Glu Asp Cys Gly His Cys
      230      235      240
Pro Ile Cys Leu Arg Pro Pro Arg Pro Gly Leu Arg Arg Gln Trp
      245      250      255

```

WO 00/44900

PCT/US00/02237

Lys Cys Val Gln Arg Arg Cys Leu Arg Gly Lys His Ala Arg Arg	260	265	270
Lys Gly Gly Cys Asp Ser Lys Met Ala Ala Arg Arg Arg Pro Gly	275	280	285
Ala Gln Pro Leu Pro Pro Pro Pro Pro Ser Gln Ser Pro Glu Pro	290	295	300
Thr Glu Pro His Pro Arg Ala Leu Ala Pro Ser Pro Pro Ala Glu	305	310	315
Phe Ile Tyr Tyr Cys Val Asp Glu Asp Glu Leu Gln Pro Tyr Thr	320	325	330
Asn Arg Arg Gln Asn Arg Lys Cys Gly Ala Cys Ala Ala Cys Leu	335	340	345
Arg Arg Met Asp Cys Gly Arg Cys Asp Phe Cys Cys Asp Lys Pro	350	355	360
Lys Phe Gly Gly Ser Asn Gln Lys Arg Gln Lys Cys Arg Trp Arg	365	370	375
Gln Cys Leu Gln Phe Ala Met Lys Arg Leu Leu Pro Ser Val Trp	380	385	390
Ser Glu Ser Glu Asp Gly Ala Gly Ser Pro Pro Pro Tyr Arg Arg	395	400	405
Arg Lys Arg Pro Ser Ser Ala Arg Arg His His Leu Gly Pro Thr	410	415	420
Leu Lys Pro Thr Leu Ala Thr Arg Thr Ala Gln Pro Asp His Thr	425	430	435
Gln Ala Pro Thr Lys Gln Glu Ala Gly Gly Gly Phe Val Leu Pro	440	445	450
Pro Pro Gly Thr Asp Leu Val Phe Leu Arg Glu Gly Ala Ser Ser	455	460	465
Pro Val Gln Val Pro Gly Pro Val Ala Ala Ser Thr Glu Ala Leu	470	475	480
Leu Gln Val Lys Gln Glu Lys Ala Asp Thr Gln Asp Glu Trp Thr	485	490	495
Pro Gly Thr Ala Val Leu Thr Ser Pro Val Leu Val Pro Gly Cys	500	505	510
Pro Ser Lys Ala Val Asp Pro Gly Leu Pro Ser Val Lys Gln Glu	515	520	525
Pro Pro Asp Pro Glu Glu Asp Lys Glu Glu Asn Lys Asp Asp Ser	530	535	540
Ala Ser Lys Leu Ala Pro Glu Glu Glu Ala Gly Gly Ala Gly Thr	545	550	555
Pro Val Ile Thr Glu Ile Phe Ser Leu Gly Gly Thr Arg Phe Arg	560	565	570
Asp Thr Ala Val Trp Leu Pro Arg Ser Lys Asp Leu Lys Lys Pro	575	580	585
Gly Ala Arg Lys Gln	590		

<210> 13
 <211> 479
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc-feature
 <223> Incyte ID No.: 1685494CD1

<400> 13
 Met Ala Thr Ala Leu Val Ser Ala His Ser Leu Ala Pro Leu Ser

1	5	10	15
Leu Lys Lys Glu Gly	Leu Arg Val Val	Arg Glu Asp His Tyr Ser	
	20	25	30
Thr Trp Glu Gln Gly	Phe Lys Leu Gln Gly	Asn Ser Lys Gly Leu	
	35	40	45
Gly Gln Glu Pro Leu	Cys Lys Gln Phe Arg	Gln Leu Arg Tyr Glu	
	50	55	60
Glu Thr Thr Gly Pro	Arg Glu Ala Leu Ser	Arg Leu Arg Glu Leu	
	65	70	75
Cys Gln Gln Trp Leu	Gln Pro Glu Thr His	Thr Lys Glu Gln Ile	
	80	85	90
Leu Glu Leu Leu Val	Leu Glu Gln Phe Leu	Ile Ile Leu Pro Lys	
	95	100	105
Glu Leu Gln Ala Arg	Val Gln Glu His His	Pro Glu Ser Arg Glu	
	110	115	120
Asp Val Val Val Val	Leu Glu Asp Leu Gln	Leu Asp Leu Gly Glu	
	125	130	135
Thr Gly Gln Gln Val	Asp Pro Asp Gln Pro	Lys Lys Gln Lys Ile	
	140	145	150
Leu Val Glu Glu Met	Ala Pro Leu Lys Gly	Val Gln Glu Gln Gln	
	155	160	165
Val Arg His Glu Cys	Glu Val Thr Lys Pro	Glu Lys Glu Lys Gly	
	170	175	180
Glu Glu Thr Arg Ile	Glu Asn Gly Lys Leu	Ile Val Val Thr Asp	
	185	190	195
Ser Cys Gly Arg Val	Glu Ser Ser Gly Lys	Ile Ser Glu Pro Met	
	200	205	210
Glu Ala His Asn Glu	Gly Ser Asn Leu Glu	Arg His Gln Ala Lys	
	215	220	225
Pro Lys Glu Lys Ile	Glu Tyr Lys Cys Ser	Glu Arg Glu Gln Arg	
	230	235	240
Phe Ile Gln His Leu	Asp Leu Ile Glu His	Ala Ser Thr His Thr	
	245	250	255
Gly Lys Lys Leu Cys	Glu Ser Asp Val Cys	Gln Ser Ser Ser Leu	
	260	265	270
Thr Gly His Lys Lys	Val Leu Ser Arg Glu	Lys Gly His Gln Cys	
	275	280	285
His Glu Cys Gly Lys	Ala Phe Gln Arg Ser	Ser His Leu Val Arg	
	290	295	300
His Gln Lys Ile His	Leu Gly Glu Lys Pro	Tyr Gln Cys Asn Glu	
	305	310	315
Cys Gly Lys Val Phe	Ser Gln Asn Ala Gly	Leu Leu Glu His Leu	
	320	325	330
Arg Ile His Thr Gly	Glu Lys Pro Tyr Leu	Cys Ile His Cys Gly	
	335	340	345
Lys Asn Phe Arg Arg	Ser Ser His Leu Asn	Arg His Gln Arg Ile	
	350	355	360
His Ser Gln Glu Glu	Pro Cys Glu Cys Lys	Glu Cys Gly Lys Thr	
	365	370	375
Phe Ser Gln Ala Leu	Leu Leu Thr His His	Gln Arg Ile His Ser	
	380	385	390
His Ser Lys Ser His	Gln Cys Asn Glu Cys	Gly Lys Ala Phe Ser	
	395	400	405
Leu Thr Ser Asp Leu	Ile Arg His His Arg	Ile His Thr Gly Glu	
	410	415	420
Lys Pro Phe Lys Cys	Asn Ile Cys Gln Lys	Ala Phe Arg Leu Asn	
	425	430	435
Ser His Leu Ala Gln	His Val Arg Ile His	Asn Glu Glu Lys Pro	
	440	445	450
Tyr Gln Cys Ser Glu	Cys Gly Glu Ala Phe	Arg Gln Arg Ser Gly	
	455	460	465
Leu Phe Gln His Gln	Arg Tyr His His Lys	Asp Lys Leu Ala	

470

475

<210> 14
 <211> 433
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc-feature
 <223> Incyte ID No.: 1730829CD1

<400> 14
 Met Glu Ala Val Tyr Leu Val Val Asn Gly Leu Gly Leu Val Leu
 1 5 10 15
 Asp Val Leu Thr Leu Val Leu Asp Leu Asn Phe Leu Leu Val Ser
 20 25 30
 Ser Leu Leu Ala Ser Leu Ala Trp Leu Leu Ala Phe Val Tyr Asn
 35 40 45
 Leu Pro His Thr Val Leu Thr Ser Leu Leu His Leu Gly Arg Gly
 50 55 60
 Val Leu Leu Ser Leu Leu Ala Leu Ile Glu Ala Val Val Arg Phe
 65 70 75
 Thr Cys Gly Gly Leu Gln Ala Leu Cys Thr Leu Leu Tyr Ser Cys
 80 85 90
 Cys Ser Gly Leu Glu Ser Leu Lys Leu Leu Gly His Leu Ala Ser
 95 100 105
 His Gly Ala Leu Arg Ser Arg Glu Ile Leu His Arg Gly Val Leu
 110 115 120
 Asn Val Val Ser Ser Gly His Ala Leu Leu Arg Gln Ala Cys Asp
 125 130 135
 Ile Cys Ala Ile Ala Met Ser Leu Val Ala Tyr Val Ile Asn Ser
 140 145 150
 Leu Val Asn Ile Cys Leu Ile Gly Thr Gln Asn Leu Phe Ser Leu
 155 160 165
 Val Leu Ala Leu Trp Asp Ala Val Thr Gly Pro Leu Trp Arg Met
 170 175 180
 Thr Asp Val Val Ala Ala Phe Leu Ala His Ile Ser Ser Ser Ala
 185 190 195
 Val Ala Met Ala Ile Leu Leu Trp Thr Pro Cys Gln Leu Ala Leu
 200 205 210
 Glu Leu Leu Ala Ser Ala Ala Arg Leu Leu Ala Ser Phe Val Leu
 215 220 225
 Val Asn Leu Thr Gly Leu Val Leu Leu Ala Cys Val Leu Ala Val
 230 235 240
 Thr Val Thr Val Leu His Pro Asp Phe Thr Leu Arg Leu Ala Thr
 245 250 255
 Gln Ala Leu Ser Gln Leu His Ala Arg Pro Ser Tyr His Arg Leu
 260 265 270
 Arg Glu Asp Val Met Arg Leu Ser Arg Leu Ala Leu Gly Ser Glu
 275 280 285
 Ala Trp Arg Arg Val Trp Ser Arg Ser Leu Gln Leu Ala Ser Trp
 290 295 300
 Pro Asn Arg Gly Gly Ala Pro Gly Ala Pro Gln Gly Asp Pro Met
 305 310 315
 Arg Val Phe Ser Val Arg Thr Arg Arg Gln Asp Thr Leu Pro Glu
 320 325 330
 Ala Gly Arg Arg Ser Glu Ala Glu Glu Glu Glu Ala Arg Thr Ile
 335 340 345
 Arg Val Thr Pro Val Arg Gly Arg Glu Arg Leu Asn Glu Glu Glu

Pro Pro Gly Gly	350	355	360
Gln Asp Pro Trp Lys		Leu Leu Lys Glu Gln Glu	
	365	370	375
Glu Arg Lys Lys	Cys Val Ile Cys Gln	Asp Gln Ser Lys Thr Val	
	380	385	390
Leu Leu Leu Pro	Cys Arg His Leu Cys	Leu Cys Gln Ala Cys Thr	
	395	400	405
Glu Ile Leu Met	Arg His Pro Val Tyr	His Arg Asn Cys Pro Leu	
	410	415	420
Cys Arg Arg Gly	Ile Leu Gln Thr Leu	Asn Val Tyr Leu	
	425	430	

<210> 15
 <211> 320
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc feature
 <223> Incyte ID No.: 1864641CD1

<400> 15

Met Pro Lys Lys Lys Thr Gly Ala Arg Lys Lys Ala Glu Asn Arg	
1 5 10 15	
Arg Glu Arg Glu Lys Gln Leu Arg Ala Ser Arg Ser Thr Ile Asp	
20 25 30	
Leu Ala Lys His Pro Cys Asn Ala Ser Met Glu Cys Asp Lys Cys	
35 40 45	
Gln Arg Arg Gln Lys Asn Arg Ala Phe Cys Tyr Phe Cys Asn Ser	
50 55 60	
Val Gln Lys Leu Pro Ile Cys Ala Gln Cys Gly Lys Thr Lys Cys	
65 70 75	
Met Met Lys Ser Ser Asp Cys Val Ile Lys His Ala Gly Val Tyr	
80 85 90	
Ser Thr Gly Leu Ala Met Val Gly Ala Ile Cys Asp Phe Cys Glu	
95 100 105	
Ala Trp Val Cys His Gly Arg Lys Cys Leu Ser Thr His Ala Cys	
110 115 120	
Ala Cys Pro Leu Thr Asp Ala Glu Cys Val Glu Cys Glu Arg Gly	
125 130 135	
Val Trp Asp His Gly Gly Arg Ile Phe Ser Cys Ser Phe Cys His	
140 145 150	
Asn Phe Leu Cys Glu Asp Asp Gln Phe Glu His Gln Ala Ser Cys	
155 160 165	
Gln Val Leu Glu Ala Glu Thr Phe Lys Cys Val Ser Cys Asn Arg	
170 175 180	
Leu Gly Gln His Ser Cys Leu Arg Cys Lys Ala Cys Phe Cys Asp	
185 190 195	
Asp His Thr Arg Ser Lys Val Phe Lys Gln Glu Lys Gly Lys Gln	
200 205 210	
Pro Pro Cys Pro Lys Cys Gly His Glu Thr Gln Glu Thr Lys Asp	
215 220 225	
Leu Ser Met Ser Thr Arg Ser Leu Lys Phe Gly Arg Gln Thr Gly	
230 235 240	
Gly Glu Glu Gly Asp Gly Ala Ser Gly Tyr Asp Ala Tyr Trp Lys	
245 250 255	
Asn Leu Ser Ser Asp Lys Tyr Gly Asp Thr Ser Tyr His Asp Glu	
260 265 270	
Glu Glu Asp Glu Tyr Glu Ala Glu Asp Asp Glu Glu Glu Glu Asp	

	275		280		285
Glu Gly Arg Lys Asp Ser Asp Thr Glu Ser Ser Asp Leu Phe Thr					
	290		295		300
Asn Leu Asn Leu Gly Arg Thr Tyr Ala Ser Gly Tyr Ala His Tyr					
	305		310		315
Glu Glu Gln Glu Asn					
	320				

<210> 16
 <211> 179
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc-feature
 <223> Incyte ID No.: 2444604CD1

<400> 16

Met Ala Ala Gly Phe Phe Gln Pro Phe Met Ser Pro Arg Phe Pro		
1 5 10 15		
Gly Gly Pro Arg Pro Thr Leu Arg Met Pro Ser Gln Pro Pro Ala		
20 25 30		
Cys Leu Pro Gly Ser Gln Pro Leu Leu Pro Gly Ala Met Glu Pro		
35 40 45		
Ser Pro Arg Ala Gln Gly His Pro Ser Met Gly Gly Pro Met Gln		
50 55 60		
Arg Val Thr Pro Pro Arg Gly Met Ala Ser Val Gly Pro Gln Ser		
65 70 75		
Tyr Gly Gly Gly Met Arg Pro Pro Pro Asn Ser Leu Ala Gly Pro		
80 85 90		
Gly Leu Pro Ala Met Asn Met Gly Pro Gly Val Arg Gly Pro Trp		
95 100 105		
Ala Ser Pro Ser Gly Asn Ser Ile Pro Tyr Ser Ser Ser Ser Pro		
110 115 120		
Gly Ser Tyr Thr Gly Pro Pro Gly Gly Gly Gly Pro Pro Gly Thr		
125 130 135		
Pro Ile Met Pro Ser Pro Gly Asp Ser Thr Asn Ser Ser Glu Asn		
140 145 150		
Met Tyr Thr Ile Met Asn Pro Ile Gly Gln Gly Ala Gly Arg Ala		
155 160 165		
Asn Phe Pro Leu Gly Pro Gly Pro Glu Gly Pro Trp Pro Pro		
170 175		

<210> 17
 <211> 494
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc-feature
 <223> Incyte ID No.: 2445008CD1

<400> 17

Met Gly Arg Lys Lys Lys Lys Gln Leu Lys Pro Trp Cys Trp Tyr		
1 5 10 15		
Cys Asn Arg Asp Phe Asp Asp Glu Lys Ile Leu Ile Gln His Gln		

WO 00/44900

PCT/US00/02237

		20						25					30	
Lys	Ala	Lys	His	Phe	Lys	Cys	His	Ile	Cys	His	Lys	Lys	Leu	Tyr
		35							40					45
Thr	Gly	Pro	Gly	Leu	Ala	Ile	His	Cys	Met	Gln	Val	His	Lys	Glu
		50							55					60
Thr	Ile	Asp	Ala	Val	Pro	Asn	Ala	Ile	Pro	Gly	Arg	Thr	Asp	Ile
		65							70					75
Glu	Leu	Glu	Ile	Tyr	Gly	Met	Glu	Gly	Ile	Pro	Glu	Lys	Asp	Met
		80							85					90
Asp	Glu	Arg	Arg	Arg	Leu	Leu	Glu	Gln	Lys	Thr	Gln	Glu	Ser	Gln
		95							100					105
Lys	Lys	Lys	Gln	Gln	Asp	Asp	Ser	Asp	Glu	Tyr	Asp	Asp	Asp	Asp
		110							115					120
Ser	Ala	Ala	Ser	Thr	Ser	Phe	Gln	Pro	Gln	Pro	Val	Gln	Pro	Gln
		125							130					135
Gln	Gly	Tyr	Ile	Pro	Pro	Met	Ala	Gln	Pro	Gly	Leu	Pro	Pro	Val
		140							145					150
Pro	Gly	Ala	Pro	Gly	Met	Pro	Pro	Gly	Ile	Pro	Pro	Leu	Met	Pro
		155							160					165
Gly	Val	Pro	Pro	Leu	Met	Pro	Gly	Met	Pro	Pro	Val	Met	Pro	Gly
		170							175					180
Met	Pro	Pro	Gly	Leu	His	His	Gln	Arg	Lys	Tyr	Thr	Gln	Ser	Phe
		185							190					195
Cys	Gly	Glu	Asn	Ile	Met	Met	Pro	Met	Gly	Gly	Met	Met	Pro	Pro
		200							205					210
Gly	Pro	Gly	Ile	Pro	Pro	Leu	Met	Pro	Gly	Met	Pro	Pro	Gly	Met
		215							220					225
Pro	Pro	Pro	Val	Pro	Arg	Pro	Gly	Ile	Pro	Pro	Met	Thr	Gln	Ala
		230							235					240
Gln	Ala	Val	Ser	Ala	Pro	Gly	Ile	Leu	Asn	Arg	Pro	Pro	Ala	Pro
		245							250					255
Thr	Ala	Thr	Val	Pro	Ala	Pro	Gln	Pro	Pro	Val	Thr	Lys	Pro	Leu
		260							265					270
Phe	Pro	Ser	Ala	Gly	Gln	Met	Gly	Thr	Pro	Val	Thr	Ser	Ser	Ser
		275							280					285
Thr	Ala	Ser	Ser	Asn	Ser	Glu	Ser	Leu	Ser	Ala	Ser	Ser	Lys	Ala
		290							295					300
Leu	Phe	Pro	Ser	Thr	Ala	Gln	Ala	Gln	Ala	Ala	Val	Gln	Gly	Pro
		305							310					315
Val	Gly	Thr	Asp	Phe	Lys	Pro	Leu	Asn	Ser	Thr	Pro	Ala	Thr	Thr
		320							325					330
Thr	Glu	Pro	Pro	Lys	Pro	Thr	Phe	Pro	Ala	Tyr	Thr	Gln	Ser	Thr
		335							340					345
Ala	Ser	Thr	Thr	Ser	Thr	Thr	Asn	Ser	Thr	Ala	Ala	Lys	Pro	Ala
		350							355					360
Ala	Ser	Ile	Thr	Ser	Lys	Pro	Ala	Thr	Leu	Thr	Thr	Thr	Ser	Ala
		365							370					375
Thr	Ser	Lys	Leu	Ile	His	Pro	Asp	Glu	Asp	Ile	Ser	Leu	Glu	Glu
		380							385					390
Arg	Arg	Ala	Gln	Leu	Pro	Lys	Tyr	Gln	Arg	Asn	Leu	Pro	Arg	Pro
		395							400					405
Gly	Gln	Ala	Pro	Ile	Gly	Asn	Pro	Pro	Val	Gly	Pro	Ile	Gly	Gly
		410							415					420
Met	Met	Pro	Pro	Gln	Pro	Gly	Ile	Pro	Gln	Gln	Gly	Met	Arg	Arg
		425							430					435
Pro	Pro	Met	Pro	Pro	His	Gly	Gln	Tyr	Gly	Gly	His	His	Gln	Gly
		440							445					450
Met	Pro	Gly	Tyr	Leu	Pro	Gly	Ala	Met	Pro	Pro	Tyr	Gly	Gln	Gly
		455							460					465
Pro	Pro	Met	Val	Pro	Pro	Tyr	Gln	Gly	Gly	Pro	Pro	Arg	Pro	Pro
		470							475					480

Met Gly Met Arg Pro Pro Val Met Ser Gln Gly Gly Arg Tyr
 485 490

<210> 18
 <211> 401
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc-feature
 <223> Incyte ID No.: 2572462CD1

<400> 18
 Met Ala Ser Ser Pro Arg Pro Lys Met Asp Ala Ile Leu Thr Glu
 1 5 10 15
 Ala Ile Lys Ala Cys Phe Gln Lys Ser Gly Ala Ser Val Val Ala
 20 25 30
 Ile Arg Lys Tyr Ile Ile His Lys Tyr Pro Ser Leu Glu Leu Glu
 35 40 45
 Arg Arg Gly Tyr Leu Leu Lys Gln Ala Leu Lys Arg Glu Leu Asn
 50 55 60
 Arg Gly Val Ile Lys Gln Val Lys Gly Lys Gly Ala Ser Gly Ser
 65 70 75
 Phe Val Val Val Gln Lys Ser Arg Lys Thr Pro Gln Lys Ser Arg
 80 85 90
 Asn Arg Lys Asn Arg Ser Ser Ala Val Asp Pro Glu Pro Gln Val
 95 100 105
 Lys Leu Glu Asp Val Leu Pro Leu Ala Phe Thr Arg Leu Cys Glu
 110 115 120
 Pro Lys Glu Ala Ser Tyr Ser Leu Ile Arg Lys Tyr Val Ser Gln
 125 130 135
 Tyr Tyr Pro Lys Leu Arg Val Asp Ile Arg Pro Gln Leu Leu Lys
 140 145 150
 Asn Ala Leu Gln Arg Ala Val Glu Arg Gly Gln Leu Glu Gln Ile
 155 160 165
 Thr Gly Lys Gly Ala Ser Gly Thr Phe Gln Leu Lys Lys Ser Gly
 170 175 180
 Glu Lys Pro Leu Leu Gly Gly Ser Leu Met Glu Tyr Ala Ile Leu
 185 190 195
 Ser Ala Ile Ala Ala Met Asn Glu Pro Lys Thr Cys Ser Thr Thr
 200 205 210
 Ala Leu Lys Lys Tyr Val Leu Glu Asn His Pro Gly Thr Asn Ser
 215 220 225
 Asn Tyr Gln Met His Leu Leu Lys Lys Thr Leu Gln Lys Cys Glu
 230 235 240
 Lys Asn Gly Trp Met Glu Gln Ile Ser Gly Lys Gly Phe Ser Gly
 245 250 255
 Thr Phe Gln Leu Cys Phe Pro Tyr Tyr Pro Ser Pro Gly Val Leu
 260 265 270
 Phe Pro Lys Lys Glu Pro Asp Asp Ser Arg Asp Glu Asp Glu Asp
 275 280 285
 Glu Asp Glu Ser Ser Glu Glu Asp Ser Glu Asp Glu Glu Pro Pro
 290 295 300
 Pro Lys Arg Arg Leu Gln Lys Lys Thr Pro Ala Lys Ser Pro Gly
 305 310 315
 Lys Ala Ala Ser Val Lys Gln Arg Gly Ser Lys Pro Ala Pro Lys
 320 325 330
 Val Ser Ala Ala Gln Arg Gly Lys Ala Arg Pro Leu Pro Lys Lys
 335 340 345

Ala Pro Pro Lys Ala Lys Thr Pro Ala Lys Lys Thr Arg Pro Ser
 350 355 360
 Ser Thr Val Ile Lys Lys Pro Ser Gly Gly Ser Ser Lys Lys Pro
 365 370 375
 Ala Thr Ser Ala Arg Lys Glu Val Lys Leu Pro Gly Lys Gly Lys
 380 385 390
 Ser Thr Met Lys Lys Ser Phe Arg Val Lys Lys
 395 400

<210> 19
 <211> 264
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> misc-feature
 <223> Incyte ID No.: 2572892CD1

<400> 19
 Met Pro Arg Ser Phe Leu Val Arg Lys Pro Ser Asp Pro Asn Arg
 1 5 10 15
 Lys Pro Asn Tyr Ser Glu Leu Gln Asp Ser Asn Pro Glu Phe Thr
 20 25 30
 Phe Gln Gln Pro Tyr Asp Gln Ala His Leu Leu Ala Ala Ile Pro
 35 40 45
 Pro Pro Glu Ile Leu Asn Pro Thr Ala Ser Leu Pro Met Leu Ile
 50 55 60
 Trp Asp Ser Val Leu Ala Pro Gln Ala Gln Pro Ile Ala Trp Ala
 65 70 75
 Ser Leu Arg Leu Gln Glu Ser Pro Arg Val Ala Glu Leu Thr Ser
 80 85 90
 Leu Ser Asp Glu Asp Ser Gly Lys Gly Ser Gln Pro Pro Ser Pro
 95 100 105
 Pro Ser Pro Ala Pro Ser Ser Phe Ser Ser Thr Ser Ala Ser Ser
 110 115 120
 Leu Glu Ala Glu Ala Tyr Ala Ala Phe Pro Gly Leu Gly Gln Val
 125 130 135
 Pro Lys Gln Leu Ala Gln Leu Ser Glu Ala Lys Asp Leu Gln Ala
 140 145 150
 Arg Lys Ala Phe Asn Cys Lys Tyr Cys Asn Lys Glu Tyr Leu Ser
 155 160 165
 Leu Gly Ala Leu Lys Met His Ile Arg Ser His Thr Leu Pro Cys
 170 175 180
 Val Cys Gly Thr Cys Gly Lys Ala Phe Ser Arg Pro Trp Leu Leu
 185 190 195
 Gln Gly His Val Arg Thr His Thr Gly Glu Lys Pro Phe Ser Cys
 200 205 210
 Pro His Cys Ser Arg Ala Phe Ala Asp Arg Ser Asn Leu Arg Ala
 215 220 225
 His Leu Gln Thr His Ser Asp Val Lys Lys Tyr Gln Cys Gln Ala
 230 235 240
 Cys Ala Arg Thr Phe Ser Arg Met Ser Leu Leu His Lys His Gln
 245 250 255
 Glu Ser Gly Cys Ser Gly Cys Pro Arg
 260

<210> 20
 <211> 153
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc-feature
 <223> Incyte ID No.: 2785674CD1

<400> 20
 Met Thr Lys Ile Lys Ala Asp Pro Asp Gly Pro Glu Ala Gln Ala
 1 5 10 15
 Glu Ala Cys Ser Gly Glu Arg Thr Tyr Gln Glu Leu Leu Val Asn
 20 25 30
 Gln Asn Pro Ile Ala Gln Pro Leu Ala Ser Arg Arg Leu Thr Arg
 35 40 45
 Lys Leu Tyr Lys Cys Ile Lys Lys Ala Val Lys Gln Lys Gln Ile
 50 55 60
 Arg Arg Gly Val Lys Glu Val Gln Lys Phe Val Asn Lys Gly Glu
 65 70 75
 Lys Gly Ile Met Val Leu Ala Gly Asp Thr Leu Pro Ile Glu Val
 80 85 90
 Tyr Cys His Leu Pro Val Met Cys Glu Asp Arg Asn Leu Pro Tyr
 95 100 105
 Val Tyr Ile Pro Ser Lys Thr Asp Leu Gly Ala Ala Ala Gly Ser
 110 115 120
 Lys Arg Pro Thr Cys Val Ile Met Val Lys Pro His Glu Glu Tyr
 125 130 135
 Gln Glu Ala Tyr Asp Glu Cys Leu Glu Glu Val Gln Ser Leu Pro
 140 145 150
 Leu Pro Leu

<210> 21
 <211> 243
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc-feature
 <223> Incyte ID No.: 2797479CD1

<400> 21
 Met Gly Asp Asp Ile Ser Thr His Ile Ala Pro Lys Glu Leu Arg
 1 5 10 15
 His Lys His Pro Ser Ser Val Asp Glu Val Ala Gln Val Val Lys
 20 25 30
 Gln Leu Arg Ile Ile Leu Gln Gln Gln Val Arg Pro Gly Glu Ser
 35 40 45
 Thr Val Leu Ala Leu Arg Pro Asn Val Gln Gln Ile Glu Ala Pro
 50 55 60
 Asp Val Ser Arg Asp Pro Arg Val Leu Gly Phe Asp Phe Pro Gly
 65 70 75
 Ser Ala Arg Ile His Glu Gly Thr His Thr Leu Glu Lys Pro Tyr
 80 85 90
 Glu Cys Lys Gln Cys Gly Lys Leu Leu Ser His Arg Ser Ser Phe
 95 100 105
 Arg Arg His Met Met Ala His Thr Gly Asp Gly Pro His Lys Cys
 110 115 120
 Thr Val Cys Gly Lys Ala Phe Asp Ser Pro Ser Val Phe Gln Arg

His Glu Arg Thr	125	His Thr Gly Glu Lys	130	Pro Tyr Glu Cys Lys	135
	140		145		150
Cys Gly Lys Ala	155	Phe Arg Thr Ser Ser	160	Ser Leu Arg Lys His	165
Thr Thr His Thr	170	Gly Glu Gln Pro Tyr	175	Lys Cys Lys Cys Gly	180
Ala Phe Ser Asp	185	Leu Phe Ser Phe Gln	190	Ser His Glu Thr Thr	195
Ser Glu Glu Glu	200	Pro Tyr Glu Cys Lys	205	Glu Cys Gly Lys Ala	210
Ser Ser Phe Lys	215	Tyr Phe Cys Arg His	220	Glu Arg Thr His Ser	225
Glu Lys Ser Tyr	230	Glu Cys Gln Ile Cys	235	Gly Lys Leu Ser Val	240
Ser Val Thr					

<210> 22
 <211> 485
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc-feature
 <223> Incyte ID No.: 2960640CD1

<400> 22

Met Arg Asp Asn Arg	Ala Val Ser Leu Cys	Gln Gln Glu Trp Met
1	5	10
Cys Pro Gly Pro	Ala Gln Arg Ala Leu Tyr	Arg Gly Ala Thr Gln
	20	25
Arg Lys Asp Ser	His Val Ser Leu Ala Thr	Gly Val Pro Trp Gly
	35	40
Tyr Glu Glu Thr	Lys Thr Leu Leu Ala Ile	Leu Ser Ser Ser Gln
	50	55
Phe Tyr Gly Lys	Leu Gln Thr Cys Gln Asn	Ser Gln Ile Tyr
	65	70
Arg Ala Met Ala	Glu Gly Leu Trp Glu Gln	Gly Phe Leu Arg Thr
	80	85
Pro Glu Gln Cys	Arg Thr Lys Phe Lys Ser	Leu Gln Leu Ser Tyr
	95	100
Arg Lys Val Arg	Arg Gly Arg Val Pro Glu	Pro Cys Ile Phe Tyr
	110	115
Glu Glu Met Asn	Ala Leu Ser Gly Ser Trp	Ala Ser Ala Pro Pro
	125	130
Met Ala Ser Asp	Ala Val Pro Gly Gln Glu	Gly Ser Asp Ile Glu
	140	145
Ala Gly Glu Leu	Asn His Gln Asn Gly Glu	Pro Thr Glu Val Glu
	155	160
Asp Gly Thr Val	Asp Gly Ala Asp Arg Asp	Glu Lys Asp Phe Arg
	170	175
Asn Pro Gly Gln	Glu Val Arg Lys Leu Asp	Leu Pro Val Leu Phe
	185	190
Pro Asn Arg Leu	Gly Phe Glu Phe Lys Asn	Glu Ile Lys Lys Glu
	200	205
Asn Leu Lys Trp	Asp Asp Ser Glu Glu Val	Glu Ile Asn Lys Ala
	215	220
Leu Gln Arg Lys	Ser Arg Gly Val Tyr Trp	His Ser Glu Leu Gln

Lys Gly Leu Glu	230	235	240
Ser Glu Pro Thr Ser Arg Arg Gln Cys Arg Asn	245	250	255
Ser Pro Gly Glu Ser Glu Glu Lys Thr Pro Ser Gln Glu Lys Met	260	265	270
Ser His Gln Ser Phe Cys Ala Arg Asp Lys Ala Cys Thr His Ile	275	280	285
Leu Cys Gly Lys Asn Cys Ser Gln Ser Val His Ser Pro His Lys	290	295	300
Pro Ala Leu Lys Leu Glu Lys Val Ser Gln Cys Pro Glu Cys Gly	305	310	315
Lys Thr Phe Ser Arg Ser Ser Tyr Leu Val Arg His Gln Arg Ile	320	325	330
His Thr Gly Glu Lys Pro His Lys Cys Ser Glu Cys Gly Lys Gly	335	340	345
Phe Ser Glu Arg Ser Asn Leu Thr Ala His Leu Arg Thr His Thr	350	355	360
Gly Glu Arg Pro Tyr Gln Cys Gly Gln Cys Gly Lys Ser Phe Asn	365	370	375
Gln Ser Ser Ser Leu Ile Val His Gln Arg Thr His Thr Gly Glu	380	385	390
Lys Pro Tyr Gln Cys Ile Val Cys Gly Lys Arg Phe Asn Asn Ser	395	400	405
Ser Gln Phe Ser Ala His Arg Arg Ile His Thr Gly Glu Ser Pro	410	415	420
Tyr Lys Cys Ala Val Cys Gly Lys Ile Phe Asn Asn Ser Ser His	425	430	435
Phe Ser Ala His Arg Lys Thr His Thr Gly Glu Lys Pro Tyr Arg	440	445	450
Cys Ser His Cys Glu Arg Gly Phe Thr Lys Asn Ser Ala Leu Thr	455	460	465
Arg His Gln Thr Val His Met Lys Ala Val Leu Ser Ser Gln Glu	470	475	480
Gly Arg Asp Ala Leu	485		

<210> 23

<211> 160

<212> PRT

<213> Homo sapiens

<220>

<221> misc-feature

<223> Incyte ID No.: 3454051CD1

<400> 23

Met Ser Trp Thr Cys Pro Arg Cys Gln Gln Pro Val Phe Phe Ala	1	5	10	15
Glu Lys Val Ser Ser Leu Gly Lys Asn Trp His Arg Phe Cys Leu	20	25	30	35
Lys Cys Glu Arg Cys His Ser Ile Leu Ser Pro Gly Gly His Ala	40	45	50	55
Glu His Asn Gly Arg Pro Tyr Cys His Lys Pro Cys Tyr Gly Ala	60	65	70	75
Leu Phe Gly Pro Arg Gly Pro Pro His Met Lys Thr Phe Thr Gly	80	85	90	

WO 00/44900

PCT/US00/02237

Glu	Lys	Val	Met	Ser	Leu	Gly	Arg	Asn	Trp	His	Arg	Pro	Cys	Leu
				95					100					105
Arg	Cys	Gln	Arg	Cys	His	Lys	Thr	Leu	Thr	Ala	Gly	Ser	His	Ala
				110					115					120
Glu	His	Asp	Gly	Val	Pro	Tyr	Cys	His	Val	Pro	Cys	Tyr	Gly	Tyr
				125					130					135
Leu	Phe	Gly	Pro	Lys	Gly	Val	Asn	Ile	Gly	Asp	Val	Gly	Cys	Tyr
				140					145					150
Ile	Tyr	Asp	Pro	Val	Lys	Ile	Lys	Phe	Lys					
				155					160					

<210> 24
 <211> 511
 <212> PRT
 <213> Homo sapiens

<220>
 <221>
 <223> Incyte ID No.: 3510640CD1

<400> 24

Met	Gln	Glu	Leu	Tyr	Ser	Thr	Pro	Ala	Ser	Arg	Leu	Asp	Ser	Phe
1				5					10					15
Val	Ala	Gln	Trp	Leu	Gln	Pro	His	Arg	Glu	Trp	Lys	Glu	Glu	Val
				20					25					30
Leu	Asp	Ala	Val	Arg	Thr	Val	Glu	Glu	Phe	Leu	Arg	Gln	Glu	His
				35					40					45
Phe	Gln	Gly	Lys	Arg	Gly	Leu	Asp	Gln	Asp	Val	Arg	Val	Leu	Lys
				50					55					60
Val	Val	Lys	Val	Gly	Ser	Phe	Gly	Asn	Gly	Thr	Val	Leu	Arg	Ser
				65					70					75
Thr	Arg	Glu	Val	Glu	Leu	Val	Ala	Phe	Leu	Ser	Cys	Phe	His	Ser
				80					85					90
Phe	Gln	Glu	Ala	Ala	Lys	His	His	Lys	Asp	Val	Leu	Arg	Leu	Ile
				95					100					105
Trp	Lys	Thr	Met	Trp	Gln	Ser	Gln	Asp	Leu	Leu	Asp	Leu	Gly	Leu
				110					115					120
Glu	Asp	Leu	Arg	Met	Glu	Gln	Arg	Val	Pro	Asp	Ala	Leu	Val	Phe
				125					130					135
Thr	Ile	Gln	Thr	Arg	Gly	Thr	Ala	Glu	Pro	Ile	Thr	Val	Thr	Ile
				140					145					150
Val	Pro	Ala	Tyr	Arg	Ala	Leu	Gly	Pro	Ser	Leu	Pro	Asn	Ser	Gln
				155					160					165
Pro	Pro	Pro	Glu	Val	Tyr	Val	Ser	Leu	Ile	Lys	Ala	Cys	Gly	Gly
				170					175					180
Pro	Gly	Asn	Phe	Cys	Pro	Phe	Phe	Ser	Glu	Leu	Gln	Arg	Asn	Phe
				185					190					195
Val	Lys	His	Arg	Pro	Thr	Lys	Leu	Lys	Ser	Leu	Leu	Arg	Leu	Val
				200					205					210
Lys	His	Trp	Tyr	Gln	Gln	Tyr	Val	Lys	Ala	Arg	Ser	Pro	Arg	Ala
				215					220					225
Asn	Leu	Pro	Pro	Leu	Tyr	Ala	Leu	Glu	Leu	Leu	Thr	Ile	Tyr	Ala
				230					235					240
Trp	Glu	Met	Gly	Thr	Glu	Glu	Asp	Glu	Asn	Phe	Met	Leu	Asp	Glu
				245					250					255
Gly	Phe	Thr	Thr	Val	Met	Asp	Leu	Leu	Leu	Glu	Tyr	Glu	Val	Ile
				260					265					270
Cys	Ile	Tyr	Trp	Thr	Lys	Tyr	Tyr	Thr	Leu	His	Asn	Ala	Ile	Ile

Glu Asp Cys Val	275	Arg Lys Gln Leu Lys	280	Lys Glu Arg Pro Ile	285
Leu Asp Pro Ala	290	Asp Pro Thr Leu Asn	295	Val Ala Glu Gly Tyr	300
Trp Asp Ile Val	305	Ala Gln Arg Ala Ser	310	Gln Cys Leu Lys Gln	315
Cys Cys Tyr Asp	320	Asn Arg Glu Asn Pro	325	Ile Ser Ser Trp Asn	330
Lys Arg Ala Arg	335	Asp Ile His Leu Thr	340	Val Glu Gln Arg Gly	345
Pro Asp Phe Asn	350	Leu Ile Val Asn Pro	355	Tyr Glu Pro Ile Arg	360
Val Lys Glu Lys	365	Ile Arg Arg Thr Arg	370	Gly Tyr Ser Gly Leu	375
Arg Leu Ser Phe	380	Gln Val Pro Gly Ser	385	Glu Arg Gln Leu Leu	390
Ser Arg Cys Ser	395	Leu Ala Lys Tyr Gly	400	Ile Phe Ser His Thr	405
Ile Tyr Leu Leu	410	Glu Thr Ile Pro Ser	415	Glu Ile Gln Val Phe	420
Lys Asn Pro Asp	425	Gly Gly Ser Tyr Ala	430	Tyr Ala Ile Asn Pro	435
Ser Phe Ile Leu	440	Gly Leu Lys Gln Gln	445	Ile Glu Asp Gln Gln	450
	455		460		465
Leu Pro Lys Lys	470	Gln Gln Gln Leu Glu	475	Phe Gln Gly Gln Val	480
Gln Asp Trp Leu	485	Gly Leu Gly Ile Tyr	490	Gly Ile Gln Asp Ser	495
Thr Leu Ile Leu	500	Ser Lys Lys Lys Gly	505	Glu Ala Leu Phe Pro	510
Ser					

<210> 25
 <211> 310
 <212> PRT
 <213> Homo sapiens

<220> -
 <223> Incyte ID No.: 3815083CD1

<400> 25

Met Arg Pro Leu Gln	1	Ile Val Pro Ser Arg	10	Leu Ile Ser Gln Leu	15
Tyr Cys Gly Leu Lys	20	Pro Pro Ala Ser Thr	25	Arg Asn Gln Ile Cys	30
Leu Lys Met Ala Arg	35	Pro Ser Ser Ser Met	40	Ala Asp Phe Arg Lys	45
Phe Phe Ala Lys Ala	50	Lys His Ile Val Ile	55	Ile Ser Gly Ala Gly	60
Val Ser Ala Glu Ser	65	Gly Val Pro Thr Phe	70	Arg Gly Ala Gly Gly	75
Tyr Trp Arg Lys Trp	80	Gln Ala Gln Asp Leu	85	Ala Thr Pro Leu Ala	90
Phe Ala His Asn Pro	95	Ser Arg Val Trp Glu	100	Phe Tyr His Tyr Arg	105
Arg Glu Val Met Gly	110	Ser Lys Glu Pro Asn	115	Ala Gly His Arg Ala	120

```

Ile Ala Glu Cys Glu Thr Arg Leu Gly Lys Gln Gly Arg Arg Val
125 130 135
Val Val Ile Thr Gln Asn Ile Asp Glu Leu His Arg Lys Ala Gly
140 145 150
Thr Lys Asn Leu Leu Glu Ile His Gly Ser Leu Phe Lys Thr Arg
155 160 165
Cys Thr Ser Cys Gly Val Val Ala Glu Asn Tyr Lys Ser Pro Ile
170 175 180
Cys Pro Ala Leu Ser Gly Lys Gly Ala Pro Glu Pro Gly Thr Gln
185 190 195
Asp Ala Ser Ile Pro Val Glu Lys Leu Pro Arg Cys Glu Glu Ala
200 205 210
Gly Cys Gly Gly Leu Leu Arg Pro His Val Val Trp Phe Gly Glu
215 220 225
Asn Leu Asp Pro Ala Ile Leu Glu Glu Val Asp Arg Glu Leu Ala
230 235 240
His Cys Asp Leu Cys Leu Val Val Gly Thr Ser Ser Val Val Tyr
245 250 255
Pro Ala Ala Met Phe Ala Pro Gln Val Ala Ala Arg Gly Val Pro
260 265 270
Val Ala Glu Phe Asn Thr Glu Thr Thr Pro Ala Thr Asn Arg Phe
275 280 285
Arg Phe His Phe Gln Gly Pro Cys Gly Thr Thr Leu Pro Glu Ala
290 295 300
Leu Ala Cys His Glu Asn Glu Thr Val Ser
305 310

```

<210> 26

<211> 331

<212> PRT

<213> Homo sapiens

<220> -

<221> misc-feature

<223> Incyte ID No.: 3988457CD1

<400> 26

```

Met Ala Ile Asn Arg Phe Arg Leu Glu Asn Asp Leu Glu Glu Leu
1 5 10 15
Ala Leu Tyr Gln Ile Gln Leu Leu Lys Asp Leu Arg His Thr Glu
20 25 30
Asn Glu Glu Asp Lys Val Ser Ser Ser Ser Phe Arg Gln Arg Met
35 40 45
Leu Gly Asn Leu Leu Arg Pro Pro Tyr Glu Arg Pro Glu Leu Pro
50 55 60
Thr Cys Leu Tyr Val Ile Gly Leu Thr Gly Ile Ser Gly Ser Gly
65 70 75
Lys Ser Ser Ile Ala Gln Arg Leu Lys Gly Leu Gly Ala Phe Val
80 85 90
Ile Asp Ser Asp His Leu Gly His Arg Ala Tyr Ala Pro Gly Gly
95 100 105
Pro Ala Tyr Gln Pro Val Val Glu Ala Phe Gly Thr Asp Ile Leu
110 115 120
His Lys Asp Gly Ile Ile Asn Arg Lys Val Leu Gly Ser Arg Val
125 130 135
Phe Gly Asn Lys Lys Gln Leu Lys Ile Leu Thr Asp Ile Met Trp
140 145 150
Pro Ile Ile Ala Lys Leu Ala Arg Glu Glu Met Asp Arg Ala Val
155 160 165
Ala Glu Gly Lys Arg Val Cys Val Ile Asp Ala Ala Val Leu Leu
170 175 180

```

Glu Ala Gly Trp Gln Asn Leu Val His Glu Val Trp Thr Ala Val
 185 190 195
 Ile Pro Glu Thr Glu Ala Val Arg Arg Ile Val Glu Arg Asp Gly
 200 205 210
 Leu Ser Glu Ala Ala Ala Gln Ser Arg Leu Gln Ser Gln Met Ser
 215 220 225
 Gly Gln Gln Leu Val Glu Gln Ser His Val Val Leu Ser Ser Pro
 230 235 240
 Cys Gly Ser Arg Ile Ser Pro Asn Ala Arg Trp Arg Lys Pro Gly
 245 250 255
 Pro Ser Cys Arg Ser Ala Phe Pro Arg Leu Ile Arg Pro Ser Thr
 260 265 270
 Glu Lys Phe Ser Val Gly Pro Asp Trp Leu Leu Glu Leu Thr Ser
 275 280 285
 Asp Pro Val Val Arg Arg Asn Gly Gly Leu Asp Ala His Pro Gly
 290 295 300
 Ser Gly Pro Glu Val Gln Ala Ile Leu Cys Arg Thr Trp Pro Gly
 305 310 315
 Leu Val Asp Thr Gly Ser Leu Pro Asn Thr Leu Val Phe Gly Gln
 320 325 330
 His

<210> 27
 <211> 200
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc-feature
 <223> Incyte ID No.: 131890CD1

<400> 27
 Met Met Thr Ala Glu Ser Arg Glu Ala Thr Gly Leu Ser Pro Gln
 1 5 10 15
 Ala Ala Gln Glu Lys Asp Gly Ile Val Ile Val Lys Val Glu Glu
 20 25 30
 Glu Asp Glu Glu Asp His Met Trp Gly Gln Asp Ser Thr Leu Gln
 35 40 45
 Asp Thr Pro Pro Pro Asp Pro Glu Ile Phe Arg Gln Arg Phe Arg
 50 55 60
 Arg Phe Cys Tyr Gln Asn Thr Phe Gly Pro Arg Glu Ala Leu Ser
 65 70 75
 Arg Leu Lys Glu Leu Cys His Gln Trp Leu Arg Pro Glu Ile Asn
 80 85 90
 Thr Lys Glu Gln Ile Leu Glu Leu Leu Val Leu Glu Gln Phe Leu
 95 100 105
 Ser Ile Leu Pro Lys Glu Leu Gln Val Trp Leu Gln Glu Tyr Arg
 110 115 120
 Pro Asp Ser Gly Glu Glu Ala Val Thr Leu Leu Glu Asp Leu Glu
 125 130 135
 Leu Asp Leu Ser Gly Gln Gln Val Pro Gly Gln Val His Gly Pro
 140 145 150
 Glu Met Leu Ala Arg Gly Met Val Pro Leu Asp Pro Val Gln Glu
 155 160 165
 Ser Ser Ser Phe Asp Leu His His Glu Ala Thr Gln Ser His Phe
 170 175 180
 Lys His Ser Ser Arg Lys Pro Arg Leu Leu Gln Ser Arg Gly Lys
 185 190 195
 Lys Gln Gly Phe Ile

WO 00/44900

PCT/US00/02237

200

<210> 28
<211> 100
<212> PRT
<213> Homo sapiens

<220>
<221> misc-feature
<223> Incyte ID No.: 238642CD1

<400> 28
Met Gln Lys Pro Cys Lys Glu Asn Glu Gly Lys Pro Lys Cys Ser
1 5 10 15
Val Pro Lys Arg Glu Glu Lys Arg Pro Tyr Gly Glu Phe Glu Arg
20 25 30
Gln Gln Thr Glu Gly Asn Phe Arg Gln Arg Leu Leu Gln Ser Leu
35 40 45
Glu Glu Phe Lys Glu Asp Ile Asp Tyr Arg His Phe Lys Asp Glu
50 55 60
Glu Met Thr Arg Glu Gly Asp Glu Met Glu Arg Cys Leu Glu Glu
65 70 75
Ile Arg Gly Leu Arg Lys Lys Phe Arg Ala Leu His Ser Asn His
80 85 90
Arg His Ser Arg Asp Arg Pro Tyr Pro Ile
95 100

<210> 29
<211> 528
<212> PRT
<213> Homo sapiens

<220>
<221> misc-feature
<223> Incyte ID No.: 669862CD1

<400> 29
Met Ser Ser Pro Tyr Pro Leu Leu Leu Glu Asn Ser Ile Cys Leu
1 5 10 15
Phe Phe His Phe Leu Pro Asp Phe Asn Phe Thr Thr Glu Ser Asn
20 25 30
Lys Leu Ser Ser Glu Lys Arg Asn Tyr Glu Val Asn Ala Tyr His
35 40 45
Gln Glu Thr Trp Lys Arg Asn Lys Thr Phe Asn Leu Met Arg Phe
50 55 60
Ile Phe Arg Thr Asp Pro Gln Tyr Thr Ile Glu Phe Gly Arg Gln
65 70 75
Gln Arg Pro Lys Val Gly Cys Phe Ser Gln Met Ile Phe Lys Lys
80 85 90
His Lys Ser Leu Pro Leu His Lys Arg Asn Asn Thr Arg Glu Lys
95 100 105
Ser Tyr Glu Cys Lys Glu Tyr Lys Lys Gly Phe Arg Lys Tyr Leu
110 115 120
His Leu Thr Glu His Leu Arg Asp His Thr Gly Val Ile Pro Tyr
125 130 135
Glu Cys Asn Glu Cys Gly Lys Ala Phe Val Val Phe Gln His Phe

WO 00/44900

PCT/US00/02237

Ile Arg His Arg	140	Ile His Thr Asp	145	Leu Lys Pro Tyr Glu Cys	150
Asn Gly Cys Glu	155	Lys Ala Phe Arg Phe	160	Tyr Ser Gln Leu Ile Gln	165
His Gln Ile Ile	170	His Thr Gly Met Lys	175	Pro Tyr Glu Cys Lys Gln	180
Cys Gly Lys Ala	185	Phe Arg Arg His Ser	190	His Leu Thr Glu His Gln	195
Lys Ile His Val	200	Gly Leu Lys Pro Phe	205	Glu Cys Lys Glu Cys Gly	210
Glu Thr Phe Arg	215	Leu Tyr Arg His Met	220	Cys Leu His Gln Lys Ile	225
His His Gly Val	230	Lys Pro Tyr Lys Cys	235	Lys Glu Cys Gly Lys Ala	240
Phe Gly His Arg	245	Ser Ser Leu Tyr Gln	250	His Lys Lys Ile His Ser	255
Gly Glu Lys Pro	260	Tyr Lys Cys Glu Gln	265	Cys Glu Lys Ala Phe Val	270
Arg Ser Tyr Leu	275	Leu Val Glu His Gln	280	Arg Ser His Thr Gly Glu	285
Lys Pro His Glu	290	Cys Met Glu Cys Gly	295	Lys Ala Phe Ser Lys Gly	300
Ser Ser Leu Leu	305	Lys His Lys Arg Ile	310	His Ser Ser Glu Lys Leu	315
Tyr Asp Cys Lys	320	Asp Cys Gly Lys Ala	325	Phe Cys Arg Gly Ser Gln	330
Leu Thr Gln His	335	Gln Arg Ile His Thr	340	Gly Glu Lys Pro His Glu	345
Cys Lys Glu Cys	350	Gly Lys Thr Phe Lys	355	Leu His Ser Tyr Leu Ile	360
Gln His Gln Ile	365	Ile His Thr Asp Leu	370	Lys Pro Tyr Glu Cys Lys	375
Gln Cys Gly Lys	380	Ala Phe Ser Arg Val	385	Gly Asp Leu Lys Thr His	390
Gln Ser Ile His	395	Ala Gly Glu Lys Pro	400	Tyr Glu Cys Lys Glu Cys	405
Gly Lys Thr Phe	410	Arg Leu Asn Ser Gln	415	Leu Ile Tyr His Gln Thr	420
Ile His Thr Gly	425	Leu Lys Pro Tyr Val	430	Cys Lys Glu Cys Lys Lys	435
Ala Phe Arg Ser	440	Ile Ser Gly Leu Ser	445	Gln His Lys Arg Ile His	450
Thr Gly Glu Lys	455	Pro Tyr Glu Cys Lys	460	Glu Cys Asp Lys Ala Phe	465
Asn Arg Ser Asp	470	Arg Leu Thr Gln His	475	Glu Thr Ile His Thr Gly	480
Val Lys Pro Gln	485	Lys Cys Lys Glu Cys	490	Gly Lys Ala Phe Ser His	495
Cys Tyr Gln Leu	500	Ser Gln His Gln Arg	505	Phe His His Gly Glu Arg	510
Leu Leu Met	515		520		525

<210> 30
 <211> 350
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc-feature
 <223> Incyte ID No.: 1003663CD1

<400> 30

```

Met His Pro Ala Ala Phe Pro Leu Pro Val Val Val Ala Ala Val
1      5      10
Leu Trp Gly Ala Ala Pro Thr Arg Gly Leu Ile Arg Ala Thr Ser
20      25      30
Asp His Asn Ala Ser Met Asp Phe Ala Asp Leu Pro Ala Leu Phe
35      40      45
Gly Ala Thr Leu Ser Gln Glu Gly Leu Gln Gly Phe Leu Val Glu
50      55      60
Ala His Pro Asp Asn Ala Cys Ser Pro Ile Ala Pro Pro Pro Pro
65      70      75
Ala Pro Val Asn Gly Ser Val Phe Ile Ala Leu Leu Arg Arg Phe
80      85      90
Asp Cys Asn Phe Asp Leu Lys Val Leu Asn Ala Gln Lys Ala Gly
95      100     105
Tyr Gly Ala Ala Val Val His Asn Val Asn Ser Asn Glu Leu Leu
110     115     120
Asn Met Val Trp Asn Ser Glu Glu Ile Gln Gln Gln Ile Trp Ile
125     130     135
Pro Ser Val Phe Ile Gly Glu Arg Ser Ser Glu Tyr Leu Arg Ala
140     145     150
Leu Phe Val Tyr Glu Lys Gly Ala Arg Val Leu Leu Val Pro Asp
155     160     165
Asn Thr Phe Pro Leu Gly Tyr Tyr Leu Ile Pro Phe Thr Gly Ile
170     175     180
Val Gly Leu Leu Val Leu Ala Met Gly Ala Val Met Ile Ala Arg
185     190     195
Cys Ile Gln His Arg Lys Arg Leu Gln Arg Asn Arg Leu Thr Lys
200     205     210
Glu Gln Leu Lys Gln Ile Pro Thr His Asp Tyr Gln Lys Gly Asp
215     220     225
Gln Tyr Asp Val Cys Ala Ile Cys Leu Asp Glu Tyr Glu Asp Gly
230     235     240
Asp Lys Leu Arg Val Leu Pro Cys Ala His Ala Tyr His Ser Arg
245     250     255
Cys Val Asp Pro Trp Leu Thr Gln Thr Arg Lys Thr Cys Pro Ile
260     265     270
Cys Lys Gln Pro Val His Arg Gly Pro Gly Asp Glu Asp Gln Glu
275     280     285
Glu Glu Thr Gln Gly Gln Glu Glu Gly Asp Glu Gly Glu Pro Arg
290     295     300
Asp His Pro Ala Ser Glu Arg Thr Pro Leu Leu Gly Ser Ser Pro
305     310     315
Thr Leu Pro Thr Ser Phe Gly Ser Leu Ala Pro Ala Pro Leu Val
320     325     330
Phe Pro Gly Pro Ser Thr Asp Pro Pro Leu Ser Pro Pro Ser Ser
335     340     345
Pro Val Ile Leu Val
350

```

<210> 31

<211> 315

<212> PRT

<213> Homo sapiens

<220>

<221> misc-feature

<223> Incyte ID No.: 1432557CD1

<400> 31

```

Met Ala Ala Leu Gly Val Leu Glu Ser Asp Leu Pro Ser Ala Val
 1          5          10          15
Thr Leu Leu Lys Asn Leu Gln Glu Gln Val Met Ala Val Thr Ala
          20          25          30
Gln Val Lys Ser Leu Thr Gln Lys Val Gln Ala Gly Ala Tyr Pro
          35          40          45
Thr Glu Lys Gly Leu Ser Phe Leu Glu Val Lys Asp Gln Leu Leu
          50          55          60
Leu Met Tyr Leu Met Asp Leu Thr His Leu Ile Leu Asp Lys Ala
          65          70          75
Ser Gly Gly Ser Leu Gln Gly His Asp Ala Val Leu Arg Leu Val
          80          85          90
Glu Ile Arg Thr Val Leu Glu Lys Leu Arg Pro Leu Asp Gln Lys
          95          100          105
Leu Lys Tyr Gln Ile Asp Lys Leu Ile Lys Thr Ala Val Thr Gly
          110          115          120
Ser Leu Ser Glu Asn Asp Pro Leu Arg Phe Lys Pro His Pro Ser
          125          130          135
Asn Met Met Ser Lys Leu Ser Ser Glu Asp Glu Glu Glu Asp Glu
          140          145          150
Ala Glu Asp Asp Gln Ser Glu Ala Ser Gly Lys Lys Ser Val Lys
          155          160          165
Gly Val Ser Lys Lys Tyr Val Pro Pro Arg Leu Val Pro Val His
          170          175          180
Tyr Asp Glu Thr Glu Ala Glu Arg Glu Lys Lys Arg Leu Glu Arg
          185          190          195
Ala Lys Arg Arg Ala Leu Ser Ser Ser Val Ile Arg Glu Leu Lys
          200          205          210
Glu Gln Tyr Ser Asp Ala Pro Glu Glu Ile Arg Asp Ala Arg His
          215          220          225
Pro His Val Thr Arg Gln Ser Gln Glu Asp Gln His Arg Ile Asn
          230          235          240
Tyr Glu Glu Ser Met Met Val Arg Leu Ser Val Ser Lys Arg Glu
          245          250          255
Lys Gly Arg Arg Lys Arg Ala Asn Val Met Ser Ser Gln Leu His
          260          265          270
Ser Leu Thr His Phe Ser Asp Ile Ser Ala Leu Thr Gly Gly Thr
          275          280          285
Val His Leu Asp Glu Asp Gln Asn Pro Ile Lys Lys Arg Lys Lys
          290          295          300
Ile Pro Gln Lys Gly Arg Lys Lys Lys Gly Phe Arg Arg Arg Arg
          305          310          315

```

<210> 32

<211> 120

<212> PRT

<213> Homo sapiens

<220>

<221> misc-feature

<223> 1441770CD1

<400> 32

```

Met Asp Asp Ser Lys Val Val Gly Gly Lys Val Lys Lys Pro Gly
 1          5          10          15
Lys Arg Gly Arg Lys Pro Ala Lys Ile Asp Leu Lys Ala Lys Leu
          20          25          30
Glu Arg Ser Arg Gln Ser Ala Arg Glu Cys Arg Ala Arg Lys Lys
          35          40          45

```

Leu	Arg	Tyr	Gln	Tyr	Leu	Glu	Glu	Leu	Val	Ser	Ser	Arg	Glu	Arg
				50					55					60
Ala	Ile	Cys	Ala	Leu	Arg	Glu	Glu	Leu	Glu	Met	Tyr	Lys	Gln	Trp
				65					70					75
Cys	Met	Ala	Met	Asp	Gln	Gly	Lys	Ile	Pro	Ser	Glu	Ile	Lys	Ala
				80					85					90
Leu	Leu	Thr	Gly	Glu	Glu	Gln	Asn	Lys	Ser	Gln	Gln	Asn	Ser	Ser
				95					100					105
Arg	His	Thr	Lys	Ala	Gly	Lys	Thr	Asp	Ala	Asn	Ser	Asn	Ser	Trp
				110					115					120

<210> 33
 <211> 326
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc-feature
 <223> Incyte ID No.: 1456684CD1

<400> 33

Met	Gln	Glu	Glu	Pro	Leu	Pro	Gln	Gly	Asn	Asp	Pro	Glu	Pro	Ser
1				5					10					15
Gly	Asp	Ser	Pro	Leu	Gly	Leu	Cys	Gln	Ser	Glu	Cys	Met	Glu	Met
				20					25					30
Ser	Glu	Val	Phe	Asp	Asp	Ala	Ser	Asp	Gln	Asp	Ser	Thr	Asp	Lys
				35					40					45
Pro	Trp	Arg	Pro	Tyr	Tyr	Asn	Tyr	Lys	Pro	Lys	Lys	Lys	Ser	Arg
				50					55					60
Gln	Leu	Lys	Lys	Met	Arg	Lys	Val	Asn	Trp	Arg	Lys	Glu	His	Gly
				65					70					75
Asn	Arg	Ser	Pro	Ser	His	Lys	Cys	Lys	Tyr	Pro	Ala	Glu	Leu	Asp
				80					85					90
Cys	Ala	Val	Gly	Lys	Ala	Pro	Gln	Asp	Lys	Pro	Phe	Glu	Glu	Glu
				95					100					105
Glu	Thr	Lys	Glu	Met	Pro	Lys	Leu	Gln	Cys	Glu	Leu	Cys	Asp	Gly
				110					115					120
Asp	Lys	Ala	Val	Gly	Ala	Gly	Asn	Gln	Gly	Arg	Pro	His	Arg	His
				125					130					135
Leu	Thr	Ser	Arg	Pro	Tyr	Ala	Cys	Glu	Leu	Cys	Ala	Lys	Gln	Phe
				140					145					150
Gln	Ser	Pro	Ser	Thr	Leu	Lys	Met	His	Met	Arg	Cys	His	Thr	Gly
				155					160					165
Glu	Lys	Pro	Tyr	Gln	Cys	Lys	Thr	Cys	Gly	Arg	Cys	Phe	Ser	Val
				170					175					180
Gln	Gly	Asn	Leu	Gln	Lys	His	Glu	Arg	Ile	His	Leu	Gly	Leu	Lys
				185					190					195
Glu	Phe	Val	Cys	Gln	Tyr	Cys	Asn	Lys	Ala	Phe	Thr	Leu	Asn	Glu
				200					205					210
Thr	Leu	Lys	Ile	His	Glu	Arg	Ile	His	Thr	Gly	Glu	Lys	Arg	Tyr
				215					220					225
His	Cys	Gln	Phe	Cys	Phe	Gln	Arg	Phe	Leu	Tyr	Leu	Ser	Thr	Lys
				230					235					240
Arg	Asn	His	Glu	Gln	Arg	His	Ile	Arg	Glu	His	Asn	Gly	Lys	Gly
				245					250					255
Tyr	Ala	Cys	Phe	Gln	Cys	Pro	Lys	Ile	Cys	Lys	Thr	Ala	Ala	Ala
				260					265					270
Leu	Gly	Met	His	Gln	Lys	Lys	His	Leu	Phe	Lys	Ser	Pro	Ser	Gln
				275					280					285

<210> 38
 <211> 445
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc-feature
 <223> Incyte ID No.: 2056207CD1

<400> 38
 Met Val Glu Cys Ile Arg Glu Val Asn Glu Val Ile Gln Asn Pro
 1 5 10 15
 Ala Thr Ile Thr Arg Ile Leu Leu Ser His Phe Asn Trp Asp Lys
 20 25 30
 Glu Lys Leu Met Glu Arg Tyr Phe Asp Gly Asn Leu Glu Lys Leu
 35 40 45
 Phe Ala Glu Cys His Val Ile Asn Pro Ser Lys Lys Ser Arg Thr
 50 55 60
 Arg Gln Met Asn Thr Arg Ser Ser Ala Gln Asp Met Pro Cys Gln
 65 70 75
 Ile Cys Tyr Leu Asn Tyr Pro Asn Ser Tyr Phe Thr Gly Leu Glu
 80 85 90
 Cys Gly His Lys Phe Cys Met Gln Cys Trp Ser Glu Tyr Leu Thr
 95 100 105
 Thr Lys Ile Met Glu Glu Gly Met Gly Gln Thr Ile Ser Cys Pro
 110 115 120
 Ala His Gly Cys Asp Ile Leu Val Asp Asp Asn Thr Val Met Arg
 125 130 135
 Leu Ile Thr Asp Ser Lys Val Lys Leu Lys Tyr Gln His Leu Ile
 140 145 150
 Thr Asn Ser Phe Val Glu Cys Asn Arg Leu Leu Lys Trp Cys Pro
 155 160 165
 Ala Pro Asp Cys His His Val Val Lys Val Gln Tyr Pro Asp Ala
 170 175 180
 Lys Pro Val Arg Cys Lys Cys Gly Arg Gln Phe Cys Phe Asn Cys
 185 190 195
 Gly Glu Asn Trp His Asp Pro Val Lys Cys Lys Trp Leu Lys Lys
 200 205 210
 Trp Ile Lys Lys Cys Asp Asp Asp Ser Glu Thr Ser Asn Trp Ile
 215 220 225
 Ala Ala Asn Thr Lys Glu Cys Pro Lys Cys His Val Thr Ile Glu
 230 235 240
 Lys Asp Gly Gly Cys Asn His Met Val Cys Arg Asn Gln Asn Cys
 245 250 255
 Lys Ala Glu Phe Cys Trp Val Cys Leu Gly Pro Trp Glu Pro His
 260 265 270
 Gly Ser Ala Trp Tyr Asn Cys Asn Arg Tyr Asn Glu Asp Asp Ala
 275 280 285
 Lys Ala Ala Arg Asp Ala Gln Glu Arg Ser Arg Ala Ala Leu Gln
 290 295 300
 Arg Tyr Leu Phe Tyr Cys Asn Arg Tyr Met Asn His Met Gln Ser
 305 310 315
 Leu Arg Phe Glu His Lys Leu Tyr Ala Gln Val Lys Gln Lys Met
 320 325 330
 Glu Glu Met Gln Gln His Asn Met Ser Trp Ile Glu Val Gln Phe
 335 340 345
 Leu Lys Lys Ala Val Asp Val Leu Cys Gln Cys Arg Ala Thr Leu
 350 355 360
 Met Tyr Thr Tyr Val Phe Ala Phe Tyr Leu Lys Lys Asn Asn Gln
 365 370 375
 Ser Ile Ile Phe Glu Asn Asn Gln Ala Asp Leu Glu Asn Ala Thr
 380 385 390

WO 00/44900

PCT/US00/02237

Glu	Val	Leu	Ser	Gly	Tyr	Leu	Glu	Arg	Asp	Ile	Ser	Gln	Asp	Ser
				395					400					405
Leu	Gln	Asp	Ile	Lys	Gln	Lys	Val	Gln	Asp	Lys	Tyr	Arg	Tyr	Cys
				410					415					420
Glu	Ser	Arg	Arg	Arg	Val	Leu	Leu	Gln	His	Val	His	Glu	Gly	Tyr
				425					430					435
Glu	Lys	Asp	Leu	Trp	Glu	Tyr	Ile	Glu	Asp					
				440					445					

<210> 39
 <211> 433
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc-feature
 <223> Incyte ID No.: 2101803CD1

<400> 39

Met	Arg	Ala	Glu	Gly	Leu	Gly	Gly	Leu	Glu	Arg	Phe	Cys	Ser	Pro
1				5					10					15
Gly	Lys	Gly	Arg	Gly	Leu	Arg	Ala	Leu	Gln	Pro	Phe	Gln	Val	Gly
				20					25					30
Asp	Leu	Leu	Phe	Ser	Cys	Pro	Ala	Tyr	Ala	Tyr	Val	Leu	Thr	Val
				35					40					45
Asn	Glu	Arg	Gly	Asn	His	Cys	Glu	Tyr	Cys	Phe	Thr	Arg	Lys	Glu
				50					55					60
Gly	Leu	Ser	Lys	Cys	Gly	Arg	Cys	Lys	Gln	Ala	Phe	Tyr	Cys	Asn
				65					70					75
Val	Glu	Cys	Gln	Lys	Glu	Asp	Trp	Pro	Met	His	Lys	Leu	Glu	Cys
				80					85					90
Ser	Pro	Met	Val	Val	Phe	Gly	Glu	Asn	Trp	Asn	Pro	Ser	Glu	Thr
				95					100					105
Val	Arg	Leu	Thr	Ala	Arg	Ile	Leu	Ala	Lys	Gln	Lys	Ile	His	Pro
				110					115					120
Glu	Arg	Thr	Pro	Ser	Glu	Lys	Leu	Leu	Ala	Val	Lys	Glu	Phe	Glu
				125					130					135
Ser	His	Leu	Asp	Lys	Leu	Asp	Asn	Glu	Lys	Lys	Asp	Leu	Ile	Gln
				140					145					150
Ser	Asp	Ile	Ala	Ala	Leu	His	His	Phe	Tyr	Ser	Lys	His	Leu	Glu
				155					160					165
Phe	Pro	Asp	Asn	Asp	Ser	Leu	Val	Val	Leu	Phe	Ala	Gln	Val	Asn
				170					175					180
Cys	Asn	Gly	Phe	Thr	Ile	Glu	Asp	Glu	Glu	Leu	Ser	His	Leu	Gly
				185					190					195
Ser	Ala	Ile	Phe	Pro	Asp	Val	Ala	Leu	Met	Asn	His	Ser	Cys	Cys
				200					205					210
Pro	Asn	Val	Ile	Val	Thr	Tyr	Lys	Gly	Thr	Leu	Ala	Glu	Val	Arg
				215					220					225
Ala	Val	Gln	Glu	Ile	Lys	Pro	Gly	Glu	Glu	Val	Phe	Thr	Ser	Tyr
				230					235					240
Ile	Asp	Leu	Leu	Tyr	Pro	Thr	Glu	Asp	Arg	Asn	Asp	Arg	Leu	Arg
				245					250					255
Asp	Ser	Tyr	Phe	Phe	Thr	Cys	Glu	Cys	Gln	Glu	Cys	Thr	Thr	Lys
				260					265					270
Asp	Lys	Asp	Lys	Ala	Lys	Val	Glu	Ile	Arg	Lys	Leu	Ser	Asp	Pro
				275					280					285
Pro	Lys	Ala	Glu	Ala	Ile	Arg	Asp	Met	Val	Arg	Tyr	Ala	Arg	Asn
				290					295					300

WO 00/44900

PCT/US00/02237

Val	Ile	Glu	Glu	Phe	Arg	Arg	Ala	Lys	His	Tyr	Lys	Ser	Pro	Ser	
				305					310					315	
Glu	Leu	Leu	Glu	Ile	Cys	Glu	Leu	Ser	Gln	Glu	Lys	Met	Ser	Ser	
				320					325					330	
Val	Phe	Glu	Asp	Ser	Asn	Val	Tyr	Met	Leu	His	Met	Met	Tyr	Gln	
				335					340					345	
Ala	Met	Gly	Val	Cys	Leu	Tyr	Met	Gln	Asp	Trp	Glu	Gly	Ala	Leu	
				350					355					360	
Gln	Tyr	Gly	Gln	Lys	Ile	Ile	Lys	Pro	Tyr	Ser	Lys	His	Tyr	Pro	
				365					370					375	
Leu	Tyr	Ser	Leu	Asn	Val	Ala	Ser	Met	Trp	Leu	Lys	Leu	Gly	Arg	
				380					385					390	
Leu	Tyr	Met	Gly	Leu	Glu	His	Lys	Ala	Ala	Gly	Glu	Lys	Ala	Leu	
				395					400					405	
Lys	Lys	Ala	Ile	Ala	Ile	Met	Glu	Val	Ala	His	Gly	Lys	Asp	His	
				410					415					420	
Pro	Tyr	Ile	Ser	Glu	Ile	Lys	Gln	Glu	Ile	Glu	Ser	His			
				425					430						

<210> 40
 <211> 355
 <212> PRT
 <213> Homo sapiens

 <220>
 <221> misc-feature
 <223> Incyte ID No.: 2112362CD1

<400> 40

Met	Ser	Val	Asn	Tyr	Ala	Ala	Gly	Leu	Ser	Pro	Tyr	Ala	Asp	Lys	
1				5					10					15	
Gly	Lys	Cys	Gly	Leu	Pro	Glu	Ile	Phe	Asp	Pro	Pro	Glu	Glu	Leu	
				20					25					30	
Glu	Arg	Lys	Val	Trp	Glu	Leu	Ala	Arg	Leu	Val	Trp	Gln	Ser	Ser	
				35					40					45	
Asn	Val	Val	Phe	His	Thr	Gly	Ala	Gly	Ile	Ser	Thr	Ala	Ser	Gly	
				50					55					60	
Ile	Pro	Asp	Phe	Arg	Gly	Pro	His	Gly	Val	Trp	Thr	Met	Glu	Glu	
				65					70					75	
Arg	Gly	Leu	Ala	Pro	Lys	Phe	Asp	Thr	Thr	Phe	Glu	Ser	Ala	Arg	
				80					85					90	
Pro	Thr	Gln	Thr	His	Met	Ala	Leu	Val	Gln	Leu	Glu	Arg	Val	Gly	
				95					100					105	
Leu	Leu	Arg	Phe	Leu	Val	Ser	Gln	Asn	Val	Asp	Gly	Leu	His	Val	
				110					115					120	
Arg	Ser	Gly	Phe	Pro	Arg	Asp	Lys	Leu	Ala	Glu	Leu	His	Gly	Asn	
				125					130					135	
Met	Phe	Val	Glu	Glu	Cys	Ala	Lys	Cys	Lys	Thr	Gln	Tyr	Val	Arg	
				140					145					150	
Asp	Thr	Val	Val	Gly	Thr	Met	Gly	Leu	Lys	Ala	Thr	Gly	Arg	Leu	
				155					160					165	
Cys	Thr	Val	Ala	Lys	Ala	Arg	Gly	Leu	Arg	Ala	Cys	Arg	Gly	Glu	
				170					175					180	
Leu	Arg	Asp	Thr	Ile	Leu	Asp	Trp	Glu	Asp	Ser	Leu	Pro	Asp	Arg	
				185					190					195	
Asp	Leu	Ala	Leu	Ala	Asp	Glu	Ala	Ser	Arg	Asn	Ala	Asp	Leu	Ser	
				200					205					210	
Ile	Thr	Leu	Gly	Thr	Ser	Leu	Gln	Ile	Arg	Pro	Ser	Gly	Asn	Leu	
				215					220					225	

```

Pro Leu Ala Thr Lys Arg Arg Gly Gly Arg Leu Val Ile Val Asn
                230                235                240
Leu Gln Pro Thr Lys His Asp Arg His Ala Asp Leu Arg Ile His
                245                250                255
Gly Tyr Val Asp Glu Val Met Thr Arg Leu Met Lys His Leu Gly
                260                265                270
Leu Glu Ile Pro Ala Trp Asp Gly Pro Arg Val Leu Glu Arg Ala
                275                280                285
Leu Pro Pro Leu Pro Arg Pro Pro Thr Pro Lys Leu Glu Pro Lys
                290                295                300
Glu Glu Ser Pro Thr Arg Ile Asn Gly Ser Ile Pro Ala Gly Pro
                305                310                315
Lys Gln Glu Pro Cys Ala Gln His Asn Gly Ser Glu Pro Ala Ser
                320                325                330
Pro Lys Arg Glu Arg Pro Thr Ser Pro Ala Pro His Arg Pro Pro
                335                340                345
Lys Arg Val Lys Ala Lys Ala Val Pro Ser
                350                355

```

```

<210> 41
<211> 443
<212> PRT
<213> Homo sapiens

<220>
<221> misc-feature
<223> Incyte ID No.: 2117346CD1

```

```

<400> 41
Met Asp Arg Leu Gly Ser Phe Ser Asn Asp Pro Ser Asp Lys Pro
  1      5      10      15
Pro Cys Arg Gly Cys Ser Ser Tyr Leu Met Glu Pro Tyr Ile Lys
      20      25      30
Cys Ala Glu Cys Gly Pro Pro Pro Phe Phe Leu Cys Leu Gln Cys
      35      40      45
Phe Thr Arg Gly Phe Glu Tyr Lys Lys His Gln Ser Asp His Thr
      50      55      60
Tyr Glu Ile Met Thr Ser Asp Phe Pro Val Leu Asp Pro Ser Trp
      65      70      75
Thr Ala Gln Glu Glu Met Ala Leu Leu Glu Ala Val Met Asp Cys
      80      85      90
Gly Phe Gly Asn Trp Gln Asp Val Ala Asn Gln Met Cys Thr Lys
      95     100     105
Thr Lys Glu Glu Cys Glu Lys His Tyr Met Lys His Phe Ile Asn
     110     115     120
Asn Pro Leu Phe Ala Ser Thr Leu Leu Asn Leu Lys Gln Ala Glu
     125     130     135
Glu Ala Lys Thr Ala Asp Thr Ala Ile Pro Phe His Ser Thr Asp
     140     145     150
Asp Pro Pro Arg Pro Thr Phe Asp Ser Leu Leu Ser Arg Asp Met
     155     160     165
Ala Gly Tyr Met Pro Ala Arg Ala Asp Phe Ile Glu Glu Phe Asp
     170     175     180
Asn Tyr Ala Glu Trp Asp Leu Arg Asp Ile Asp Phe Val Glu Asp
     185     190     195
Asp Ser Asp Ile Leu His Ala Leu Lys Met Ala Val Val Asp Ile
     200     205     210
Tyr His Ser Arg Leu Lys Glu Arg Gln Arg Arg Lys Lys Ile Ile
     215     220     225

```

PCT/US00/02237

Arg	Asp	His	Gly	Leu 230	Ile	Asn	Leu	Arg	Lys 235	Phe	Gln	Leu	Met	Glu 240
Arg	Arg	Tyr	Pro	Lys 245	Glu	Val	Gln	Asp	Leu 250	Tyr	Glu	Thr	Met	Arg 255
Arg	Phe	Ala	Arg	Ile 260	Val	Gly	Pro	Val	Glu 265	His	Asp	Lys	Phe	Ile 270
Glu	Ser	His	Ala	Leu 275	Glu	Phe	Glu	Leu	Arg 280	Arg	Glu	Ile	Lys	Arg 285
Leu	Gln	Glu	Tyr	Arg 290	Thr	Ala	Gly	Ile	Thr 295	Asn	Phe	Cys	Ser	Ala 300
Arg	Thr	Tyr	Asp	His 305	Leu	Lys	Lys	Thr	Arg 310	Glu	Glu	Glu	Arg	Leu 315
Lys	Arg	Thr	Met	Leu 320	Ser	Glu	Val	Leu	Gln 325	Tyr	Ile	Gln	Asp	Ser 330
Ser	Ala	Cys	Gln	Gln 335	Trp	Leu	Arg	Arg	Gln 340	Ala	Asp	Ile	Asp	Ser 345
Gly	Leu	Ser	Pro	Ser 350	Ile	Pro	Met	Ala	Ser 355	Asn	Ser	Gly	Arg	Arg 360
Ser	Ala	Pro	Pro	Leu 365	Asn	Leu	Thr	Gly	Leu 370	Pro	Gly	Thr	Glu	Lys 375
Leu	Asn	Glu	Lys	Glu 380	Lys	Glu	Leu	Cys	Gln 385	Met	Val	Arg	Leu	Val 390
Pro	Gly	Ala	Tyr	Leu 395	Glu	Tyr	Lys	Ser	Ala 400	Leu	Leu	Asn	Glu	Cys 405
Asn	Lys	Gln	Gly	Gly 410	Leu	Arg	Leu	Ala	Gln 415	Ala	Arg	Ala	Leu	Ile 420
Lys	Ile	Asp	Val	Asn 425	Lys	Thr	Arg	Lys	Ile 430	Tyr	Asp	Phe	Leu	Ile 435
Arg	Glu	Gly	Tyr	Ile 440	Thr	Lys	Gly							

```
<210> 42
<211> 164
<212> PRT
<213> Homo sapiens

<220>
<221> misc-feature
<223> Incyte ID No.: 2119917CD1
```

<400> 42														
Met	Thr	Ala	Ser	Ala	Gln	Pro	Arg	Gly	Arg	Arg	Pro	Gly	Val	Gly
1				5					10					15
Val	Gly	Val	Val	Val	Thr	Ser	Cys	Lys	His	Pro	Arg	Cys	Val	Leu
				20					25					30
Leu	Gly	Lys	Arg	Lys	Gly	Ser	Val	Gly	Ala	Gly	Ser	Phe	Gln	Leu
				35					40					45
Pro	Gly	Gly	His	Leu	Glu	Phe	Gly	Glu	Thr	Trp	Glu	Glu	Cys	Ala
				50					55					60
Gln	Arg	Glu	Thr	Trp	Glu	Glu	Ala	Ala	Leu	His	Leu	Lys	Asn	Val
				65					70					75
His	Phe	Ala	Ser	Val	Val	Asn	Ser	Phe	Ile	Glu	Lys	Glu	Asn	Tyr
				80					85					90
His	Tyr	Val	Thr	Ile	Leu	Met	Lys	Gly	Glu	Val	Asp	Val	Thr	His
				95					100					105
Asp	Ser	Glu	Pro	Lys	Asn	Val	Glu	Pro	Glu	Lys	Asn	Glu	Ser	Trp
				110					115					120
Glu	Trp	Val	Pro	Trp	Glu	Glu	Leu	Pro	Pro	Leu	Asp	Gln	Leu	Phe
				125					130					135

Trp Gly Leu Arg Cys Leu Lys Glu Gln Gly Tyr Asp Pro Phe Lys
 140 145 150
 Glu Asp Leu Asn His Leu Val Gly Tyr Lys Gly Asn His Leu
 155 160

<210> 43
 <211> 215
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc-feature
 <223> Incyte ID No.: 2123456CD1

<400> 43
 Met Leu Gly Ala Glu Trp Ser Lys Leu Gln Pro Thr Glu Lys Gln
 1 5 10 15
 Arg Tyr Leu Asp Glu Ala Glu Arg Glu Lys Gln Gln Tyr Met Lys
 20 25 30
 Glu Leu Arg Ala Tyr Gln Gln Ser Glu Ala Tyr Lys Met Cys Thr
 35 40 45
 Glu Lys Ile Gln Glu Lys Lys Ile Lys Lys Glu Asp Ser Ser Ser
 50 55 60
 Gly Leu Met Asn Thr Leu Leu Asn Gly His Lys Gly Gly Asp Cys
 65 70 75
 Asp Gly Phe Ser Thr Phe Asp Val Pro Ile Phe Thr Glu Glu Phe
 80 85 90
 Leu Asp Gln Asn Lys Ala Arg Glu Ala Glu Leu Arg Arg Leu Arg
 95 100 105
 Lys Met Asn Val Ala Phe Glu Glu Gln Asn Ala Val Leu Gln Arg
 110 115 120
 His Thr Gln Ser Met Ser Ser Ala Arg Glu Arg Leu Glu Gln Glu
 125 130 135
 Leu Ala Leu Glu Glu Arg Arg Thr Leu Ala Leu Gln Gln Gln Leu
 140 145 150
 Gln Ala Val Arg Gln Ala Leu Thr Ala Ser Phe Ala Ser Leu Pro
 155 160 165
 Val Pro Gly Thr Gly Glu Thr Pro Thr Leu Gly Thr Leu Asp Phe
 170 175 180
 Tyr Met Ala Arg Leu His Gly Ala Ile Glu Arg Asp Pro Ala Gln
 185 190 195
 His Glu Lys Leu Ile Val Arg Ile Lys Glu Ile Leu Ala Gln Val
 200 205 210
 Ala Ser Glu His Leu
 215

<210> 44
 <211> 539
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc-feature
 <223> Incyte ID No.: 2148792CD1

<400> 44

Met	Ala	Ala	Leu	Phe	Leu	Ser	Ala	Pro	Pro	Gln	Ala	Glu	Val	Thr
1				5					10					15
Phe	Glu	Asp	Val	Ala	Val	Tyr	Leu	Ser	Arg	Glu	Glu	Trp	Gly	Arg
				20					25					30
Leu	Gly	Pro	Ala	Gln	Arg	Gly	Leu	Tyr	Arg	Asp	Val	Met	Leu	Glu
				35					40					45
Thr	Tyr	Gly	Asn	Leu	Val	Ser	Leu	Gly	Val	Gly	Pro	Ala	Gly	Pro
				50					55					60
Lys	Pro	Gly	Val	Ile	Ser	Gln	Leu	Glu	Arg	Gly	Asp	Glu	Pro	Trp
				65					70					75
Val	Leu	Asp	Val	Gln	Gly	Thr	Ser	Gly	Lys	Glu	His	Leu	Arg	Val
				80					85					90
Asn	Ser	Pro	Ala	Leu	Gly	Thr	Arg	Thr	Glu	Tyr	Lys	Glu	Leu	Thr
				95					100					105
Ser	Gln	Glu	Thr	Phe	Gly	Glu	Glu	Asp	Pro	Gln	Gly	Ser	Glu	Pro
				110					115					120
Val	Glu	Ala	Cys	Asp	His	Ile	Ser	Lys	Ser	Glu	Gly	Ser	Leu	Glu
				125					130					135
Lys	Leu	Val	Glu	Gln	Arg	Gly	Pro	Arg	Ala	Val	Thr	Leu	Thr	Asn
				140					145					150
Gly	Glu	Ser	Ser	Arg	Glu	Ser	Gly	Gly	Asn	Leu	Arg	Leu	Leu	Ser
				155					160					165
Arg	Pro	Val	Pro	Asp	Gln	Arg	Pro	His	Lys	Cys	Asp	Ile	Cys	Glu
				170					175					180
Gln	Ser	Phe	Glu	Gln	Arg	Ser	Tyr	Leu	Asn	Asn	His	Lys	Arg	Val
				185					190					195
His	Arg	Ser	Lys	Lys	Thr	Asn	Thr	Val	Arg	Asn	Ser	Gly	Glu	Ile
				200					205					210
Phe	Ser	Ala	Asn	Leu	Val	Val	Lys	Glu	Asp	Gln	Lys	Ile	Pro	Thr
				215					220					225
Gly	Lys	Lys	Leu	His	Tyr	Cys	Ser	Tyr	Cys	Gly	Lys	Thr	Phe	Arg
				230					235					240
Tyr	Ser	Ala	Asn	Leu	Val	Lys	His	Gln	Arg	Leu	His	Thr	Glu	Glu
				245					250					255
Lys	Pro	Tyr	Lys	Cys	Asp	Glu	Cys	Gly	Lys	Ala	Phe	Ser	Gln	Ser
				260					265					270
Cys	Glu	Phe	Ile	Asn	His	Arg	Arg	Met	His	Ser	Gly	Glu	Ile	Pro
				275					280					285
Tyr	Arg	Cys	Asp	Glu	Cys	Gly	Lys	Thr	Phe	Thr	Arg	Arg	Pro	Asn
				290					295					300
Leu	Met	Lys	His	Gln	Arg	Ile	His	Thr	Gly	Glu	Lys	Pro	Tyr	Lys
				305					310					315
Cys	Gly	Glu	Cys	Gly	Lys	His	Phe	Ser	Ala	Tyr	Ser	Ser	Leu	Ile
				320					325					330
Tyr	His	Gln	Arg	Ile	His	Thr	Gly	Glu	Lys	Pro	Tyr	Lys	Cys	Asn
				335					340					345
Asp	Cys	Gly	Lys	Ala	Phe	Ser	Asp	Gly	Ser	Ile	Leu	Ile	Arg	His
				350					355					360
Arg	Arg	Thr	His	Thr	Gly	Glu	Lys	Pro	Phe	Glu	Cys	Lys	Glu	Cys
				365					370					375
Gly	Lys	Gly	Phe	Thr	Gln	Ser	Ser	Asn	Leu	Ile	Gln	His	Gln	Arg
				380					385					390
Ile	His	Thr	Gly	Glu	Lys	Pro	Tyr	Lys	Cys	Asn	Glu	Cys	Glu	Lys
				395					400					405
Ala	Phe	Ile	Gln	Lys	Thr	Lys	Leu	Val	Glu	His	Gln	Arg	Ser	His
				410					415					420
Thr	Gly	Glu	Lys	Pro	Tyr	Glu	Cys	Asn	Asp	Cys	Gly	Lys	Val	Phe
				425					430					435
Ser	Gln	Ser	Thr	His	Leu	Ile	Gln	His	Gln	Arg	Ile	His	Thr	Gly
				440					445					450
Glu	Lys	Pro	Tyr	Lys	Cys	Ser	Glu	Cys	Gly	Lys	Ala	Phe	His	Asn
				455					460					465

```

Ser Ser Arg Leu Ile His His Gln Arg Leu His His Gly Glu Lys
      470      475      480
Pro Tyr Arg Cys Ser Asp Cys Lys Lys Ala Phe Ser Gln Ser Thr
      485      490      495
Tyr Leu Ile Gln His Arg Arg Ile His Thr Gly Glu Lys Pro Tyr
      500      505      510
Lys Cys Ser Glu Cys Gly Lys Ala Phe Arg His Ser Ser Asn Met
      515      520      525
Cys Gln His Gln Arg Ile His Leu Arg Glu Asp Phe Ser Met
      530      535

```

<210> 45
 <211> 182
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc-feature
 <223> Incyte ID No.: 2751943CD1

```

<400> 45
Met Ala Arg Leu Leu Trp Leu Leu Arg Gly Leu Thr Leu Gly Thr
  1      5      10      15
Ala Pro Arg Arg Ala Val Arg Gly Gln Ala Gly Gly Gly Gly Pro
      20      25      30
Gly Thr Gly Pro Gly Leu Gly Glu Ala Gly Ser Leu Ala Thr Cys
      35      40      45
Glu Leu Pro Leu Ala Lys Ser Glu Trp Gln Lys Lys Leu Thr Pro
      50      55      60
Glu Gln Phe Tyr Val Thr Arg Glu Lys Gly Thr Glu Pro Pro Phe
      65      70      75
Ser Gly Ile Tyr Leu Asn Asn Lys Glu Ala Gly Met Tyr His Cys
      80      85      90
Val Cys Cys Asp Ser Pro Leu Phe Ser Ser Glu Lys Lys Tyr Cys
      95      100      105
Ser Gly Thr Gly Trp Pro Ser Phe Ser Glu Ala His Gly Thr Ser
      110      115      120
Gly Ser Asp Glu Ser His Thr Gly Ile Leu Arg Arg Leu Asp Thr
      125      130      135
Ser Leu Gly Ser Ala Arg Thr Glu Val Val Cys Lys Gln Cys Glu
      140      145      150
Ala His Leu Gly His Val Phe Pro Asp Gly Pro Gly Pro Asn Gly
      155      160      165

Gln Arg Phe Cys Ile Asn Ser Val Ala Leu Lys Phe Lys Pro Arg
      170      175      180
Lys His

```

<210> 46
 <211> 534
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc-feature
 <223> Incyte ID No.: 3128913CD1

<400> 46

Met	Ala	Val	Glu	Ser	Gly	Val	Ile	Ser	Thr	Leu	Ile	Pro	Gln	Asp	
1				5					10					15	
Pro	Pro	Glu	Gln	Glu	Leu	Ile	Leu	Val	Lys	Val	Glu	Asp	Asn	Phe	
				20					25					30	
Ser	Trp	Asp	Glu	Lys	Phe	Lys	Gln	Asn	Gly	Ser	Thr	Gln	Ser	Cys	
				35					40					45	
Gln	Glu	Leu	Phe	Arg	Gln	Gln	Phe	Arg	Lys	Phe	Cys	Tyr	Gln	Glu	
				50					55					60	
Thr	Pro	Gly	Pro	Arg	Glu	Ala	Leu	Ser	Arg	Leu	Gln	Glu	Leu	Cys	
				65					70					75	
Tyr	Gln	Trp	Leu	Met	Pro	Glu	Leu	His	Thr	Lys	Glu	Gln	Ile	Leu	
				80					85					90	
Glu	Leu	Leu	Val	Leu	Glu	Gln	Phe	Leu	Ser	Ile	Leu	Pro	Glu	Glu	
				95					100					105	
Leu	Gln	Ile	Trp	Val	Gln	Gln	His	Asn	Pro	Glu	Ser	Gly	Glu	Glu	
				110					115					120	
Ala	Val	Thr	Leu	Leu	Glu	Asp	Leu	Glu	Arg	Glu	Phe	Asp	Asp	Pro	
				125					130					135	
Gly	Gln	Gln	Val	Pro	Ala	Ser	Pro	Gln	Gly	Pro	Ala	Val	Pro	Trp	
				140					145					150	
Lys	Asp	Leu	Thr	Cys	Leu	Arg	Ala	Ser	Gln	Glu	Ser	Thr	Asp	Ile	
				155					160					165	
His	Leu	Gln	Pro	Leu	Lys	Thr	Gln	Leu	Lys	Ser	Trp	Lys	Pro	Cys	
				170					175					180	
Leu	Ser	Pro	Lys	Ser	Asp	Cys	Glu	Asn	Ser	Glu	Thr	Ala	Thr	Lys	
				185					190					195	
Glu	Gly	Ile	Ser	Glu	Glu	Lys	Ser	Gln	Gly	Leu	Pro	Gln	Glu	Pro	
				200					205					210	
Ser	Phe	Arg	Gly	Ile	Ser	Glu	His	Glu	Ser	Asn	Leu	Val	Trp	Lys	
				215					220					225	
Gln	Gly	Ser	Ala	Thr	Gly	Glu	Lys	Leu	Arg	Ser	Pro	Ser	Gln	Gly	
				230					235					240	
Gly	Ser	Phe	Ser	Gln	Val	Ile	Phe	Thr	Asn	Lys	Ser	Leu	Gly	Lys	
				245					250					255	
Arg	Asp	Leu	Tyr	Asp	Glu	Ala	Glu	Arg	Cys	Leu	Ile	Leu	Thr	Thr	
				260					265					270	
Asp	Ser	Ile	Met	Cys	Gln	Lys	Val	Pro	Pro	Glu	Glu	Arg	Pro	Tyr	
				275					280					285	
Arg	Cys	Asp	Val	Cys	Gly	His	Ser	Phe	Lys	Gln	His	Ser	Ser	Leu	
				290					295					300	
Thr	Gln	His	Gln	Arg	Ile	His	Thr	Gly	Glu	Lys	Pro	Tyr	Lys	Cys	
				305					310					315	
Asn	Gln	Cys	Gly	Lys	Ala	Phe	Ser	Leu	Arg	Ser	Tyr	Leu	Ile	Ile	
				320					325					330	
His	Gln	Arg	Ile	His	Ser	Gly	Glu	Lys	Ala	Tyr	Glu	Cys	Ser	Glu	
				335					340					345	
Cys	Gly	Lys	Ala	Phe	Asn	Gln	Ser	Ser	Ala	Leu	Ile	Arg	His	Arg	
				350					355					360	
Lys	Ile	His	Thr	Gly	Glu	Lys	Ala	Cys	Lys	Cys	Asn	Glu	Cys	Gly	
				365					370					375	
Lys	Ala	Phe	Ser	Gln	Ser	Ser	Tyr	Leu	Ile	Ile	His	Gln	Arg	Ile	
				380					385					390	
His	Thr	Gly	Glu	Lys	Pro	Tyr	Glu	Cys	Asn	Glu	Cys	Gly	Lys	Thr	
				395					400					405	
Phe	Ser	Gln	Ser	Ser	Lys	Leu	Ile	Arg	His	Gln	Arg	Ile	His	Thr	
				410					415					420	
Gly	Glu	Arg	Pro	Tyr	Glu	Cys	Asn	Glu	Cys	Gly	Lys	Ala	Phe	Arg	
				425					430					435	
Gln	Ser	Ser	Glu	Leu	Ile	Thr	His	Gln	Arg	Ile	His	Ser	Gly	Glu	
				440					445					450	
Lys	Pro	Tyr	Glu	Cys	Ser	Glu	Cys	Gly	Lys	Ala	Phe	Ser	Leu	Ser	

	455		460		465
Ser Asn Leu Ile Arg	His Gln Arg Ile	His Ser Gly Glu Glu	Pro		
	470		475		480
Tyr Gln Cys Asn Glu	Cys Gly Lys Thr	Phe Lys Arg Ser Ser	Ala		
	485		490		495
Leu Val Gln His Gln	Arg Ile His Ser	Gly Asp Glu Ala Tyr	Ile		
	500		505		510
Cys Asn Glu Cys Gly	Lys Ala Phe Arg	His Arg Ser Val Leu	Met		
	515		520		525
Arg His Gln Arg Val	His Thr Ile Lys				
	530				

<210> 47
 <211> 206
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc-feature
 <223> Incyte ID No.: 3282941CD1

<400> 47

Met Ser Thr Gly Ser Val Ser Asp Pro Glu Glu Met Glu Leu Arg	
1 5 10 15	
Gly Leu Gln Arg Glu Tyr Pro Val Pro Ala Ser Lys Arg Pro Pro	
20 25 30	
Leu Arg Gly Val Glu Arg Ser Tyr Ala Ser Pro Ser Asp Asn Ser	
35 40 45	
Ser Ala Glu Glu Glu Asp Pro Asp Gly Glu Glu Glu Arg Cys Ala	
50 55 60	
Leu Gly Thr Ala Gly Ser Ala Glu Gly Cys Lys Arg Lys Arg Pro	
65 70 75	
Arg Val Ala Gly Gly Gly Gly Ala Gly Gly Ser Ala Gly Gly Gly	
80 85 90	
Gly Lys Lys Pro Leu Pro Ala Lys Gly Ser Ala Ala Glu Cys Lys	
95 100 105	
Gln Ser Gln Arg Asn Ala Ala Asn Ala Arg Glu Arg Ala Arg Met	
110 115 120	
Arg Val Leu Ser Lys Ala Phe Ser Arg Leu Lys Thr Ser Leu Pro	
125 130 135	
Trp Val Pro Pro Asp Thr Lys Leu Ser Lys Leu Asp Thr Leu Arg	
140 145 150	
Leu Ala Ser Ser Tyr Ile Ala His Leu Arg Gln Leu Leu Gln Glu	
155 160 165	
Asp Arg Tyr Glu Asn Gly Tyr Val His Pro Val Asn Leu Thr Trp	
170 175 180	
Pro Phe Val Val Ser Gly Arg Pro Asp Ser Asp Thr Lys Glu Val	
185 190 195	
Ser Ala Ala Asn Arg Leu Cys Gly Thr Thr Ala	
200 205	

<210> 48
 <211> 172
 <212> PRT
 <213> Homo sapiens

Lys Val Phe His	140	Lys Phe Ser Asn Ser	145	Asn Thr Tyr Lys Thr	150
	155		160		165
His Thr Gly Ile	170	Asn Leu Phe Lys Cys	175	Ile Ile Cys Gly Lys	180
	185		190		195
Phe Lys Arg Ser	200	Ser Thr Leu Thr Thr	205	His Lys Lys Ile His	210
	215		220		225
Gly Glu Lys Pro	230	Tyr Lys Cys Glu Glu	235	Cys Gly Lys Ala Phe	240
	245		250		255
Gln Ser Ser Asn	260	Leu Thr Thr His Lys	265	Arg Ile His Thr Gly	270
	275				
Lys Pro Tyr Lys		Cys Glu Glu Cys Gly		Lys Ala Phe Asn Trp	
Ser Asp Leu Asn		Lys His Lys Lys Ile		His Ile Glu Arg Lys	
Tyr Ile Val Lys		Asn Val Thr Asp Leu		Leu Asn Val Pro Pro	
Leu Ile Ser Ile		Arg			

<210> 50

<211> 236

<212> PRT

<213> Homo sapiens

<220>

<221> misc-feature

<223> Incyte ID No.: 3507366CD1

<400> 50

Met Asp Lys Arg Tyr	1	Leu Gln Phe Asp Ile	10	Lys Ala Phe Val Glu	15
	5		20		30
Asn Asn Pro Ala Ile	25	Lys Trp Cys Pro Thr	35	Pro Gly Cys Asp Arg	45
	35		40		55
Ala Val Arg Leu Thr	45	Lys Gln Gly Ser Asn	55	Thr Ser Gly Ser Asp	65
	55		65		75
Thr Leu Ser Phe Pro	65	Leu Leu Arg Ala Pro	75	Ala Val Asp Cys Gly	85
	75		85		95
Lys Gly His Leu Phe	85	Cys Trp Glu Cys Leu	95	Gly Glu Ala His Glu	105
	95		105		115
Pro Cys Asp Cys Gln	105	Thr Trp Lys Asn Trp	115	Leu Gln Lys Ile Thr	125
	115		125		135
Glu Met Lys Pro Glu	125	Glu Glu Leu Val Gly	135	Val Ser Glu Ala Tyr	145
	135		145		155
Asp Ala Ala Asn Cys	145	Leu Trp Leu Leu Thr	155	Asn Ser Lys Pro Cys	165
	155		165		175
Ala Asn Cys Lys Ser	165	Pro Ile Gln Lys Asn	175	Glu Gly Cys Asn His	185
	175		185		195
Met Gln Cys Ala Lys	185	Cys Lys Tyr Asp Phe	195	Cys Trp Ile Cys Leu	205
	195		205		215
Glu Glu Trp Lys Lys	205	His Ser Ser Ser Thr	215	Gly Gly Tyr Tyr Arg	225
	215		225		235
Cys Thr Arg Tyr Glu	225	Val Ile Gln His Val	235	Glu Glu Gln Ser Lys	245
	235		245		255
Glu Met Thr Val Glu	245	Ala Glu Lys Lys His	255	Lys Arg Phe Gln Glu	265
	255		265		275
Leu Asp Arg Phe Met	265	His Tyr Tyr Thr Arg	275	Phe Lys Asn His Glu	285
	275		285		295
His Ser Tyr Gln Leu	285	Glu Gln Arg Leu Leu	295	Lys Thr Ala Lys Glu	305

215 220 225
 Lys Met Glu Gln Met Ser Arg Val Ser Lys Asn
 230 235

<210> 51
 <211> 214
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc-feature
 <223> Incyte ID No.: 3573060CD1

<400> 51
 Met Asn Leu Ser Ser Ala Ser Ser Thr Glu Glu Lys Ala Val Thr
 1 5 10 15
 Thr Val Leu Trp Gly Cys Glu Leu Ser Gln Glu Arg Arg Thr Trp
 20 25 30
 Thr Phe Arg Pro Gln Leu Glu Gly Lys Gln Ser Cys Arg Leu Leu
 35 40 45
 Leu His Thr Ile Cys Leu Gly Glu Lys Ala Lys Glu Glu Met His
 50 55 60
 Arg Val Glu Ile Leu Pro Pro Ala Asn Gln Glu Asp Lys Lys Met
 65 70 75
 Gln Pro Val Thr Ile Ala Ser Leu Gln Ala Ser Val Leu Pro Met
 80 85 90
 Val Ser Met Val Gly Val Gln Leu Ser Pro Pro Val Thr Phe Gln
 95 100 105
 Leu Arg Ala Gly Ser Gly Pro Val Phe Leu Ser Gly Gln Glu Arg
 110 115 120
 Tyr Glu Ala Ser Asp Leu Thr Trp Glu Glu Glu Glu Glu Glu
 125 130 135
 Gly Glu Glu Glu Glu Glu Glu Glu Glu Asp Asp Glu Asp Glu Asp
 140 145 150
 Ala Asp Ile Ser Leu Glu Glu Gln Ser Pro Val Lys Gln Val Lys
 155 160 165
 Arg Leu Val Pro Gln Lys Gln Ala Ser Val Ala Lys Lys Lys Lys
 170 175 180
 Leu Glu Lys Glu Glu Glu Glu Ile Arg Ala Ser Val Arg Asp Lys
 185 190 195
 Ser Pro Val Lys Lys Ala Lys Ala Thr Ala Arg Ala Lys Lys Pro
 200 205 210
 Gly Phe Lys Lys

<210> 52
 <211> 396
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc-feature
 <223> Incyte ID No.: 3573661CD1

<400> 52
 Met Asn Phe Thr Val Gly Phe Lys Pro Leu Leu Gly Asp Ala His

1	5	10	15
Ser Met Asp Asn Leu	Glu Lys Gln Leu Ile	Cys Pro Ile Cys Leu	
20	25	30	
Glu Met Phe Ser Lys	Pro Val Val Ile Leu	Pro Cys Gln His Asn	
35	40	45	
Leu Cys Arg Lys Cys	Ala Asn Asp Val Phe	Gln Ala Ser Asn Pro	
50	55	60	
Leu Trp Gln Ser Arg	Gly Ser Thr Thr Val	Ser Ser Gly Gly Arg	
65	70	75	
Phe Arg Cys Pro Ser	Cys Arg His Glu Val	Val Leu Asp Arg His	
80	85	90	
Gly Val Tyr Gly Leu	Gln Arg Asn Val Leu	Val Glu Asn Ile Ile	
95	100	105	
Asp Ile Tyr Lys Gln	Glu Ser Ser Lys Pro	Leu His Ser Lys Ala	
110	115	120	
Glu Gln His Leu Met	Cys Glu Glu His Glu	Glu Glu Lys Ile Asn	
125	130	135	
Ile Tyr Cys Leu Ser	Cys Glu Val Pro Thr	Cys Ser Leu Cys Lys	
140	145	150	
Val Phe Gly Ala His	Lys Asp Cys Glu Val	Ala Pro Leu Pro Thr	
155	160	165	
Ile Tyr Lys Arg Gln	Lys Ser Glu Leu Ser	Asp Gly Ile Ala Met	
170	175	180	
Leu Val Ala Gly Asn	Asp Arg Val Gln Ala	Val Ile Thr Gln Met	
185	190	195	
Glu Glu Val Cys Gln	Thr Ile Glu Asp Asn	Ser Arg Arg Gln Lys	
200	205	210	
Gln Leu Leu Asn Gln	Arg Phe Glu Ser Leu	Cys Ala Val Leu Glu	
215	220	225	
Glu Arg Lys Gly Glu	Leu Leu Gln Ala Leu	Ala Arg Glu Gln Glu	
230	235	240	
Glu Lys Leu Gln Arg	Val Arg Gly Leu Ile	Arg Gln Tyr Gly Asp	
245	250	255	
His Leu Glu Ala Ser	Ser Lys Leu Val Glu	Ser Ala Ile Gln Ser	
260	265	270	
Met Glu Glu Pro Gln	Met Ala Leu Tyr Leu	Gln Gln Ala Lys Glu	
275	280	285	
Leu Ile Asn Lys Val	Gly Ala Met Ser Lys	Val Glu Leu Ala Gly	
290	295	300	
Arg Pro Glu Pro Gly	Tyr Glu Ser Met Glu	Gln Phe Thr Val Arg	
305	310	315	
Val Glu His Val Ala	Glu Met Leu Arg Thr	Ile Asp Phe Gln Pro	
320	325	330	
Gly Ala Ser Gly Gly	Gly Arg Gly Gly Gly	Pro Arg Arg Lys Lys	
335	340	345	
Arg Ala Thr Arg Gly	Pro Glu Glu Lys Thr	Ala Arg Met Gly Pro	
350	355	360	
Tyr Arg Pro Leu Arg	Pro Asn Pro Asp Pro	Leu Leu Arg Lys Ser	
365	370	375	
Pro Arg Arg Leu Arg	Ile Ser Gly Gly Arg	Asn Ser Cys Arg Lys	
380	385	390	
Lys Thr Pro Ala Ser	Phe		
395			

<210> 53
 <211> 486
 <212> PRT
 <213> Homo sapiens

<220>

<221> misc-feature

<223> Incyte ID No.: 3633422CD1

<400> 53

Met	Arg	Arg	Leu	Val	His	Asp	Leu	Leu	Pro	Pro	Glu	Val	Cys	Ser
1				5					10					15
Leu	Leu	Asn	Pro	Ala	Ala	Ile	Tyr	Ala	Asn	Asn	Glu	Ile	Ser	Leu
				20					25					30
Arg	Asp	Val	Glu	Val	Tyr	Gly	Phe	Asp	Tyr	Asp	Tyr	Thr	Leu	Ala
				35					40					45
Gln	Tyr	Ala	Asp	Ala	Leu	His	Pro	Glu	Ile	Phe	Ser	Thr	Ala	Arg
				50					55					60
Asp	Ile	Leu	Ile	Glu	His	Tyr	Lys	Tyr	Pro	Glu	Gly	Ile	Arg	Lys
				65					70					75
Tyr	Asp	Tyr	Asn	Pro	Ser	Phe	Ala	Ile	Arg	Gly	Leu	His	Tyr	Asp
				80					85					90
Ile	Gln	Lys	Ser	Leu	Leu	Met	Lys	Ile	Asp	Ala	Phe	His	Tyr	Val
				95					100					105
Gln	Leu	Gly	Thr	Ala	Tyr	Arg	Gly	Leu	Gln	Pro	Val	Pro	Asp	Glu
				110					115					120
Glu	Val	Ile	Glu	Leu	Tyr	Gly	Gly	Thr	Gln	His	Ile	Pro	Leu	Tyr
				125					130					135
Gln	Met	Ser	Gly	Phe	Tyr	Gly	Lys	Gly	Pro	Ser	Ile	Lys	Gln	Phe
				140					145					150
Met	Asp	Ile	Phe	Ser	Leu	Pro	Glu	Met	Ala	Leu	Leu	Ser	Cys	Val
				155					160					165
Val	Asp	Tyr	Phe	Leu	Gly	His	Ser	Leu	Glu	Phe	Asp	Gln	Ala	His
				170					175					180
Leu	Tyr	Lys	Asp	Val	Thr	Asp	Ala	Ile	Arg	Asp	Val	His	Val	Lys
				185					190					195
Gly	Leu	Met	Tyr	Gln	Trp	Ile	Glu	Gln	Asp	Met	Glu	Lys	Tyr	Ile
				200					205					210
Leu	Arg	Gly	Asp	Glu	Thr	Phe	Ala	Val	Leu	Ser	Arg	Leu	Val	Ala
				215					220					225
His	Gly	Lys	Gln	Leu	Phe	Leu	Ile	Thr	Asn	Ser	Pro	Phe	Ser	Phe
				230					235					240
Val	Asp	Lys	Gly	Met	Arg	His	Met	Val	Gly	Pro	Asp	Trp	Arg	Gln
				245					250					255
Leu	Phe	Asp	Val	Val	Ile	Val	Gln	Ala	Asp	Lys	Pro	Ser	Phe	Phe
				260					265					270
Thr	Asp	Arg	Arg	Lys	Pro	Phe	Arg	Lys	Leu	Asp	Glu	Lys	Gly	Ser
				275					280					285
Leu	Gln	Trp	Asp	Arg	Ile	Thr	Arg	Leu	Glu	Lys	Gly	Lys	Ile	Tyr
				290					295					300
Arg	Gln	Gly	Asn	Leu	Phe	Asp	Phe	Leu	Arg	Leu	Thr	Glu	Trp	Arg
				305					310					315
Gly	Pro	Arg	Val	Leu	Tyr	Phe	Gly	Asp	His	Leu	Tyr	Ser	Asp	Leu
				320					325					330
Ala	Asp	Leu	Met	Leu	Arg	His	Gly	Trp	Arg	Thr	Gly	Ala	Ile	Ile
				335					340					345
Pro	Glu	Leu	Glu	Arg	Glu	Ile	Arg	Ile	Ile	Asn	Thr	Glu	Gln	Tyr
				350					355					360
Met	His	Ser	Leu	Thr	Trp	Gln	Gln	Ala	Leu	Thr	Gly	Leu	Leu	Glu
				365					370					375
Arg	Met	Gln	Thr	Tyr	Gln	Asp	Ala	Glu	Ser	Arg	Gln	Val	Leu	Ala
				380					385					390
Ala	Trp	Met	Lys	Glu	Arg	Gln	Glu	Leu	Arg	Cys	Ile	Thr	Lys	Ala
				395					400					405
Leu	Phe	Asn	Ala	Gln	Phe	Gly	Ser	Ile	Phe	Arg	Thr	Phe	His	Asn
				410					415					420
Pro	Thr	Tyr	Phe	Ser	Arg	Arg	Leu	Val	Arg	Phe	Ser	Asp	Leu	Tyr

SUBSTITUTE SHEET (RULE 26)

SUBSTITUTE SHEET (RULE 26)

<210> 56
<211> 2781
<212> DNA
<213> Homo sapiens

<220>
<221> misc-feature
<223> Incyte ID No.: 025733CB1

<400> 56
gaagtggggt gcacgcttcg ggttgggtgc atggcagctg cggggagccg caagaggcgc 60
ctggcggagc tgacgggtgga cgagttccta gcttcgggct ttgactccga gtccgaatcc 120
gagtcggaaa attctccaca agcggagaca cgggaagcac gcgaggctgc ccggagtcgc 180
gataagccgg gcgggagccc ctcgccagc cggcgtaaag gccgtgcctc tgagcacaaa 240
gaccagctct ctcggtgaa ggacagagac cccgagttct acaagttcct gcaggagaat 300
gaccagagcc tgctaaactt cagcgactcg gacagctctg aggaggaaga ggggcccgttc 360
cactccctgc cagatgtgct ggaggaagcc agtgaggagg aggatggagc ggaggaagga 420
gaagatgggg acagagtccc cagagggctg aaggggaaga agaattctgt tctgtgacc 480
gtcgccatgg ttgagagatg gaagcaggca gctgtcctgc gcctcactcc aaagctgttc 540
catgaagtgg tacaggcggt cagagcagct gtggccacca cccgagggga ccaggaaagt 600
gctgaggcca acaaattcca ggtaacggac agtgctgcat tcaatgctct ggttaccttc 660
tgcacagag acctcattgg ctgtctccag aagctgctgt ttggaaaagg ggcaaaaggat 720
agcagcagga tgctgcagcc gtccagcagc ccgctctggg ggaagcttcg tgtggacatc 780
aaggcttacc tgggctcggc catacagctg gtgtcctgtc tgctggagac gacggtgttg 840
gcggccgtgc tgccgcatgc tgctcaagag aatgggtggc gtgcccctgt tctgacctt cccaagcag 900
gtgctggctt tctgtgctc cagcagagtc tgccggcaca agaaggacac tttccttggc 1020
ccgctcctca agcaaatgt catcacgtat gtgaggaact gcaagttcac ctgcccgtgt 1080
gcctccctct tcatcagtt catgcagtgg accttgacgg agctgctggc cctggagccg 1140
ggtgtggcct accagcacgc ctctctctac atccgccagc tcgccataca cctgcgcaac 1200
gccatgacca cccgcaagaa ggaaacatac cagtctgtgt acaactggca gtatgtgcac 1260
tgccctcttc tgtgggtgccc ggtcctgagc actgcggggc ccagcgaagc cctccagccc 1320
ttggtctacc cccttgccca agtcatcatt ggctgtatca agctcatccc cactgcccgc 1380
ttctaccgc tgcaatgca ctgcctcgt gccctgacgc tgctctcggg gagctcgggg 1440
gccttcctcc cgggtgctgc tttcctctct gagatgttcc agcaggtcga cttcaacagg 1500
aagccagggc gcatgagct caagcccatc aacttctccg tgatcctgaa gctgtccaat 1560
gtcaacctgc aggagaaggc gtaccgggac ggcctgggtg agcagctgta cgacctcacc 1620
ctggagtacc tgcacagcca ggcacactgc atcggtctcc cggagctggt gctgcctgtg 1680
gtcctgcagc tgaagtctt cctccgggag tgcaagggtg ccaactactg ccggcagggtg 1740
cagcagctgc ttgggaagg tccaggagaac tcggcataca tctgcagccg ccgcccaggg 1800
gtttccttcg gcgtctctga gcagcaggca gtggaagcct gggagaagct gacccgggaa 1860
gaggggacac ccttgacct gtactacagc cactggcgca agctgcgtga ccgggagatc 1920
cagctggaga tcagtggcaa agagcggctg gaagacctga acttcctga gatcaaacga 1980
aggaagatgg ctgacaggaa ggatgaggac aggaagcaat ttaaagacct ctttgacctg 2040
aacagctctg aagaggacga caccgaggga ttctcgaga gagggatact gagggccctg 2100
agcactcggc atggggtgga agacgatgaa gaggacgagg aggagggcga ggaggacagc 2160
agcaactcgg aggggtgaat gtcttgggat ggagaccag acgcagaggc ggggctggcc 2220
cctggggagc tgcagcagct ggcccagggg ccggaggacg agctggagga tctgcagctc 2280
tcagaggacg actgaggcag cccatctggg gggcctgtag gggctgcccg gctgggtggc 2340
agtgtttcca cctccctggc agtcaggcct agaggctggc gtctgtgcag ttgggggagg 2400
cagtagacac gggacaggct ttattattta tttttcagca tgaagacca aacgtatcga 2460
gagctgggct gggctgggct ggtgtggctg ctgaagcccc acagctgtgg gctgctgaag 2520
tcagctccgc gggggagctg accctgacgt cagcagaccg agaccagtcc cagtccagg 2580
gggaggcctg caggccctgc gcccttcca ccacctctgc cctccgtctg cagacctcgt 2640
ccatctgcac caggtctctgc ctctactccc ccaagtcttt gaaaatttgt tcttttctct 2700
tgaagtcaca ttttctttta aaattttttg ttttgcaccc gaaaccgaaa gaaataaagg 2760
ggtgggaggc aaaaaaaaaa a 2781

<210> 57
<211> 2544
<212> DNA

WO 00/44900

PCT/US00/02237

<213> Homo sapiens

<220>

<221> misc-feature

<223> Incyte ID No.: 079702CB1

<400> 57

```

cgggaaacca aaatggcgag gggctgtatt gaagtgggct gtgtttgagg ccggtgtaag 60
aacgctcatt ctacccccaa cccttgtctc caaggacctc ggtttgtgcg tgcataatgtg 120
ccgggtaccc ggtggggcgg gtgccagta agtgctcgga ctgcaggagg aagcgccac 180
ggggacggat tggttgtttt ttctgtatg aagcggttgg caccactgaa gtgaccgaat 240
gagagactct acaggggcag gtaattcact ggtccacaag cgggtctcct tacgtcgaaa 300
ccaaaagacc ccaacatcct tgaccaagct gtctttacag gatggacata aagccaaaaa 360
gccagcatgt aaatttgaag agggtcagga tgtcctagct agatgggtcag atggcttgtt 420
ttatcttggc actatcaaaa agataaacat attgaaacag agctgcttca tcatatttga 480
agacagttct aaatcctggg ttctctggaa ggacattcaa acaggagcca ctggaagtgg 540
ggaaatggtc tgtacaatat gtcaagaaga gtattcagaa gctcccaatg aaatggttat 600
atgtgacaag tgtggccaag gatatcatca gttgtgtcac acacctcata ttgattccag 660
tgtgattgat tcagatgaaa aatggctctg tcggcagtggt gtttttgcaa caacacaaa 720
gaggggtggt gcacttaaga aaggacaaa tgccaaagca ttgcaagtca tgaagcagac 780
attaccctat agtgtggcag acctgaatg ggatgcaggt cataaaacca atgtccagca 840
gtgttactgc tattgtggag gccctggaga ctggtatttg aagatgctac agtgctgcaa 900
atgtaagcag tggtttcatg aggtctgtgt gcaatgcctt caaaagccaa tgctatttgg 960
agacagattt tatacgttta tatgctctgt ctgcagttct ggaccagaat acctcaaacg 1020
tctaccatta cagtgggtag atatagcaca cctatgcctt tacaacctaa gtgttattca 1080
taagaagaaa tactttgatt ctgaacttga gcttatgaca tacattaatg aaaactggga 1140
tagattgcac cctggagagc tggcagacac accaaaatct gaaagatatg agcatgttct 1200
ggaggcatta aatgattaca agaccatggt tatgtctggg aaagaaataa agaagaagaa 1260
gcatttgggt ttcgtgttcc tctgtgtcca ccaaattgtg ctttcaaagc 1320
agagaaagaa cctgaaggaa catctcatga atttaaaatt aaaggcagaa aggcattcaa 1380
acctatatct gattcaaggg aagtaagcaa tggcatagaa aaaaaaaaaa aaaaaaatc 1440
tgtaggctcg ccacctggcc catatacaag aaaaatgatt caaaaaactg ctgagccact 1500
tttgataag gaatcaattt cagagaatcc tactttggat ttaccttgtt ctatagggag 1560
aactgagga actgcacatt catccaatac ctccagatgtg gatttcacgg gtgcttccag 1620
tgcaaaagaa actacctcgt cttagcatttc caggcattat ggattatctg actccagaaa 1680
aagaacgcgt acaggaagat ctggcctgct tgcaatacca catttgcgga gaagaagagg 1740
tcgtcttcca agaagagcac tccagactca gaactcagaa attgtaaaaag atgatgaagg 1800
caaagaagat tatcagtttg atgaactcaa cacagagatt ctgaataact tagcagatca 1860
ggagttacaa ctcaatcatc taaagaactc cattaccagt tattttgggt ctgcaggtag 1920
aatagcatgt ggcgaaaaat accgagtttt ggcacgtcgg gtgacacttg atggaaaggt 1980
gcagtatctt gtggaatggg aaggagcaac tgcactcctga ctgtaggact gaacattatg 2040
ttcactgcac tctgattttc ttaggttaca gttcaaagcc ctaaaggagt ctggctttta 2100
ctatctttct taaaaaaaaa aaaaagtcaa aaaaattcaa aaaaggggat gatactagcc 2160
ttaacatgta cctgtcaatg ttatggatat tgtcataaaa aggtatcttt taaaaatcag 2220
aacagagact taatttttta aatcttaaga ttgtagaat gtttctagga taggatatta 2280
aaaatgattg aaacctatgc atgggtgttag acaatttttc taattattcc attgagtcag 2340
ttttttgtga ttagtgatta tcagagcaaa catcatgtag atagcacaag tatttggaga 2400
aacgttgttt gttttgttac caaaatgttg gaaaaattta tttcaatacc ttttagattt 2460
cataaagtgc agtgatatata atgctactg aaagactgta aaatattgaa attttctttc 2520
aagcaaagtg taaataaata tatc 2544

```

<210> 58

<211> 1627

<212> DNA

<213> Homo sapiens

<220>

<221> misc-feature

<223> Incyte ID No.: 116208CB1

<400> 58

<400> 61
 ttccgggttct gtaccccccat cttttctctc gccctctcta cccgcagctc ctggcgctcg 60
 gcgggggctaa ctgcagcggg gagatctcgg ccgccaagct ccgcctcccg ccccgggctg 120
 tgccccgggg ctgccttgag gccgaccacc cgcaaccac ctctagcggc tttgctcgag 180
 gcccaccttc tccccacccc cggcaaacctc cagtaggctc gccctcgctg actccccgc 240
 cccgcgtcaa ctgcaagggg cccgcccata gccagttccg gggcggttgc tcacatcgac 300
 cggaactccc cgccccctcc cgcgggccct ggggcgctag gaggccgcag cgaggaggta 360
 gagggggcgg gggtcgact aggggtgtccc tagagaacga ggactctgaa ggcgggacat 420
 ttgggcgacc cccgggcggg gccagccatt aaacagtcct actctgtgc cagacactga 480
 actgggctct tgacgggcat catctcttaa tctcagaac atcccaggga gctccacagg 540
 atccccatat cctgggccat gaggtagttg aaagactgcc ccttgcagtt ccacgacttc 600
 aagtctgttg atcacctgaa ggtctgtccc cgctacacgg cagtgtctggc acgctctgag 660
 gatgatggca tggcatcga ggagctggac accctgcagc tggagctgga gaccctgctg 720
 tctctgcca gccggcgcc cgtgtgtctt gaggccgaaa cccagatcct caccgactgg 780
 caggataaga aagggtgacag acgattcctg aagctgggtc gagaccatga acttgaggct 840
 cccccaaac atgggaagcc caagaagcag aaactggaag ggaaggcagg acatgggccc 900
 ggccctggcc caggacggcc caaatccaaa aaccttcagc ccaagatcca ggaatatgaa 960
 ttcactgatg accctatcga cgtgccacgg atccccaaaa atgatgcccc caacaggttc 1020
 tgggcttcag tggagcccta ctgtgctgac atcaccagcg aggaggctccg cacacttgag 1080
 gagttactga agcccccaga agatgaggct gagcattaca agatcccacc cctggggaag 1140
 cactactccc agcgtcgggc ccaggaggac ctgctggagg agcagaagga tggggcccgg 1200
 gcagcggtcg tggctgacaa gaagaaaggc ctcattggggc cactgaccga actggacact 1260
 aaagatgttg atgcccgtct gaagaagtct gaggccagc atgaacagcc ggaagatgga 1320
 tgcccccttg gtgcccctgac gcagcgccct ctgcaggccc tgggtggagga aaatattatt 1380
 tccccctatg aggtattctc tattcctgac atgtctggga aagaatcagg ggctgacggg 1440
 gcaagcacct cccctcgcaa tcagaacaag cccttcagtg tgccgcatac taagtccctg 1500
 gagagccgca tcaaggagga gctaattgcc cagggccttt tggagtctga ggaccgcccc 1560
 gcagaggact ccgaggatga ggtccttctg gagcttcgca aacggcaggc tgagctgaag 1620
 gcacttagtg cccaagaacc caccagctgc tgaggctggc aaaggaggag 1680
 gtgagccggc aggtgctgag gcagcgggtg cgcattggctg acaacgaggt catggacgcc 1740
 tttcgcaaga tcatggctgc ccggcagaag aagcggactc ccaccaagaa agaaaaggac 1800
 caggcctgga agactctgaa ggagcgtgag agcatcctga agctgctgga tgggtagccc 1860
 tcacccctgc ctgaggtga ttatctggcc taggggaggg gaaggagggc ccacttctct 1920
 ctttgggcac aggaacatt ggctgtggc tgtccctcaa atggcggcag tctctagagg 1980
 gccgtggccc tccccctgag gtcttttggc ctgactctgt acaaccagga cacaggaagc 2040
 cctgtgggc tagcctgagg cctagtctct gcttgggtccc cgagatgggg ttggagggga 2100
 cttegtttct ggggtcttct cttccccctt ttaccatccc ccactcccta atccccctacc 2160
 cctgtctccc ctccaaggac ttctcccttg tggttttgta aagtgcaaac ttaagaataa 2220
 agtgactgct gtgggttttc aaaaaaaaaa aaaaaa 2255

<210> 62
 <211> 2982
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc-feature
 <223> Incyte ID No.: 491271CB1

<400> 62
 gcgtggggat gtttaccgcc gtttatccgg gatagagact ccacgtgtct gacagcatcc 60
 ttttattcac cgcctccgaa tttgcaaaga ggaggaagga gggacttctt ggcttctccc 120
 agcatagccc cagttatgcc atctcagaac tatgacctc cccagaagaa gcaggagaaa 180
 atgaccaagt ttcaggaggc tgtgacatc aaggatgtgg ctgtggctct ctcaggagg 240
 gaactgcgac tgctcgatct taccagagg aagctgtacc gagatgtcat ggtggagaac 300
 ttcaagaacc tggttgcagt ggggcatctt cccttccaac cagatatggt atcccaattg 360
 gaagcagaag aaaagctttg gatgatggaa acagaaaccc aaagaagcag caagcatcaa 420
 aataagatgg aaacactcca aaaatttgca ttaaaatacc tttcaaatca agagctgtcc 480
 tgctggcaaa tctggaaaca ggttgcaagt gaattaacca ggtgtcttca ggggaagagt 540
 tcccagttat tacaagggtga ctctattcag gtttctgaaa atgagaacaa tataatgaac 600
 cctaaaggag atagccctat ttatattgaa aatcaagagt ttccattttg gagaaccag 660

SUBSTITUTE SHEET (RULE 26)

WO 00/44900

PCT/US00/02237

ctcactgggat	cgtgagacca	ggactgaaaa	tgatcaagaa	atttctgaag	acacaagatc	600
acatgggggtc	ctactgggaa	gattttcaaaa	ggatattttct	caggggtctca	agtttaaaga	660
agcctatgaa	cgagaagtca	gtctgaaaag	gccgctgggg	aactccctcg	gagaaagact	720
gaacaggaaa	atgccagatt	ttgggtcaagt	gacagttgag	gagaagctaa	ccccaggggg	780
agagagaagc	gagaaatata	atgatttttg	gaacagcttc	actgtgaatt	ccaaccttat	840
ctcacatcag	agactccccg	tgggagacag	accccataag	tgtgatgaat	gtagcaagag	900
ctttaatcga	acttcagacc	ttattcaaca	tcagagaatc	cacactgggg	aaaagcccta	960
tgaatgtaat	gagtgtggga	aggccttcag	ccagagctca	caccttattc	agcatcagag	1020
aatccacact	ggggaaaaaac	cttatgaatg	tagtgattgt	gggaaaacct	tcagctgtag	1080
ctctgccctc	attctgcatc	ggaggatcca	cacgggggag	aaacctatg	aatgtaatga	1140
gtgtgggaag	accttcagct	ggagctccac	cctcaccac	catcagagaa	tccacactgg	1200
tgagaaaccc	tacgcctgca	atgaatgtgg	gaaggccttc	agcaggagct	caacctttat	1260
tcaccatcag	agaatccaca	ctggagaaaa	acccatgaa	tgtaatgaat	gtgggaaagc	1320
cttcagccag	agctcacacc	tctatcagca	ccagagaatc	cacactggag	agaagcccta	1380
cgaatgtatg	gaatgtggag	gaaagtttac	ctacagttca	ggccttattc	agcatcaaag	1440
aatccacacc	ggggagaacc	cctatgaatg	tagtgagtgt	gggaaagcct	tcaggtagac	1500
ctcggtctct	gttcgccatc	agagaattca	cactggagag	aagcctttga	atgggatcgg	1560
gagccacaca	agctccctca	gagttacgac	cgagttaaat	atcagagagt	ccacgtgaaa	1620
aaatctcaac	agcttaggat	tgagtctcaa	tgagtctcaa	gagctcttgc	cttaccctat	1680
gcagatgggg	caaatcggtg	gtgtcccttt	caactcagac	ttttcatttt	agagaatggg	1740
gcaagtggat	ggcgtgctgg	aattttccca	gaaatcacac	cagccttaga	aagcgtcaag	1800
aaggagtgtg	cactaaactg	gaatagaaag	cagctctggg	accagttacc	ccatttagga	1860
aagcacagtc	gggacagaat	tttttctcac	agcagaggaa	cctttccaag	gtggggatgg	1920
gacagcagtg	gaaaggacgc	tcgatggatt	cctttagtgt	gagtcgcgt	agtcagcaca	1980
atttcaaagc	tactgttctt	tctgggtcct	gttatttgct	agggagggtg	aaggagact	2040
ttcatgattt	cgtttaattat	agtcacagct	taagtttcgg	taagaaacat	gctgttttgt	2100
gagattccag	aatcatcatc	ggaaattttg	cattgaggga	ttattttatt	gagggtagaa	2160
ccatgttttc	aagagaaaac	tgtgatgatg	gtgtccttta	gggctcttgg	agcagccaga	2220
tgtcctgggg	ctgaatgggc	tggtgatatt	gccagcagac	cccttgcct	ccccccagt	2280
ggtcagaagc	acttagcggt	aaatctgtcc	aaacagctag	taaccggctg	tgaggagag	2340
aatgatgaaa	atgattttct	ggcctctgat	tgctgtcctc	tcttgctcct	ttcccactcc	2400
gcctgcttgc	cctgcctctc	ctaaatgcct	gggtaaggat	gctttcaagg	agctcacttg	2460
ctccacctct	gactcttcag	cacctctgac	acccagcccc	aggagccaga	ccactcctgc	2520
ggagaaaaaa	aaaaaa	cagctgaaga	ttaatgcaga	gaaagagcaa	agcccaaaag	2580
						2596

<210> 66

<211> 1574

<212> DNA

<213> Homo sapiens

<220>

<221> misc-feature

<223> Incyte ID No.: 1443262CB1

<400> 66

cagccccgtga	gacgcccgtc	gctggacgcg	ggtagccgtc	tgagggtgccg	gagctgcggg	60
aggatgggagc	cgctgaaggt	ggaaaagttc	gcaaccgcca	acaggggaaa	cgggctgcgc	120
gccgtgaccc	cgctgcgccc	cggagagcta	ctcttcgcgt	cggatccctt	ggcgtacacg	180
gtgtgcaagg	ggagtctgtg	cgctcgtctg	gaccgctgcc	ttctcgggaa	ggaaaagctg	240
atgcgatgct	ctcagtgcgg	cgctcgccaa	tactgtagtg	ctaagtgtca	gaaaaaagct	300
tggccagacc	acaagcggga	atgcaaagtc	cttaaaagct	gcaaaccag	atatectcca	360
gactccgttc	gacttcttgg	cagagtgttc	ttcaaactta	tggatggagc	accttcagaa	420
tcagagaagc	tttactcatt	ttatgatctg	gagtcaaata	ttaacaaact	gactgaagat	480
aagaaagagg	gcctcaggca	actcgtaatg	acatttcaac	atttcatgag	agaagaaata	540
caggatgcct	ctcagctgcc	acctgccttt	gacctttttg	aagcctttgc	aaaagtgatc	600
tgcaactctt	tcaccatctg	taatgcggag	atgcaggaag	ttggtgttgg	cctatatccc	660
agtatctctt	tgtccaatca	cagctgtgac	cccaactgtt	cgattgtgtt	caatgggccc	720
cacctcttac	tgcgagcagt	ccgagacatc	gaggtgggag	aggagctcac	catctgctac	780
ctggatatgc	tgatgaccag	tgaggagcgc	cggaagcagc	tgagggacca	gtactgcttt	840
gaatgtgact	gtttccgttg	ccaaaccag	gacaaggatg	ctgatatgct	aactggtgat	900

WO 00/44900

PCT/US00/02237

gagcaagtat	ggaaggaagt	tcaagaatcc	ctgaaaaaaa	ttgaagaact	gaaggcacac	960
tggaagtggg	agcagggttct	ggccatgtgc	caggcgatca	taagcagcaa	ttctgaacgg	1020
cttccccgata	tcaacatcta	ccagctgaag	gtgctcgact	gcgccatgga	tgccctgcac	1080
aacctcgccc	tggtggagga	agccttggtc	tatggtactc	ggaccatgga	gccatacagg	1140
atTTTTTTcc	caggaagcca	tcccgtcaga	ggggttcaag	tgatgaaagt	tggcaaactg	1200
cagctacatc	aaggcatggt	tccccaaagca	atgaagaatc	tgagactggc	ttttgatatt	1260
atgagagtga	cacatggcag	agaacacagc	ctgattgaag	atTTtgattct	actTTtagaa	1320
gaatgcgcag	ccaacatcag	agcatcctaa	gggaacgcag	tcagagggaa	atacggcggtg	1380
tgtcttttgt	gaatgcctta	ttgaggtcac	acactctatg	ctttgttagc	tgtgtgaacc	1440
tctctatttg	gaaattctgt	tccgtgtttg	tgtaggtaaa	taaaggcaga	catgggttgc	1500
aaaccacaag	aatcattagt	tgtagagaag	cacgattata	ataaattcaa	aacatttggt	1560
tgaaaaaaa	aaaa					1574

<210> 67
 <211> 2197
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc-feature
 <223> Incyte ID No.: 1521648CB1

<400> 67						
cccgaacgaac	gcgaggagg	cgaggcgagg	ggtgcaggag	ggaccctcgc	catgggtcca	60
cgggcctaga	gtggcggaag	ataccggcct	ggtgccaaac	tggctactgc	tgcttccgtg	120
ggcctccatg	gctgaggact	ggctggactg	cccggccctg	ggccctggct	ggaagcgccg	180
cgaagtcttt	cgcaagtcag	gggccacctg	tggaacgtca	gacacctatt	accagagccc	240
cacaggagac	aggatccgaa	gcaaagtgtg	gctgactcga	tacctggggc	ctgctgtgga	300
tctcaccttc	ttcgacttca	aacaaggcat	cttgtgctat	ccagccccc	aggcccatcc	360
cgtggcggtt	gccagcaaga	agcgaaagaa	gccttcaagg	ccagccaaga	ctcggaacg	420
tcaggttga	ccccagagt	gtgaggtcag	gaaggaggcc	ccgagggatg	agaccaaggc	480
tgacactgac	acagccccag	cttcattccc	tgtctcctgg	tgctgtgaga	actgtggaat	540
cagcttctca	ggggatggca	cccaaaggca	gcggctcaaa	acgttgtgca	aagactgtcg	600
agcacagaga	attgccttca	accgggaaca	gagaatgttt	aagcgtgtgg	gctgtgggga	660
gtgtgcagcc	tgccaggtaa	cagaagactg	tggggcctgc	tccacctgcc	tcctgcagct	720
gccccatgat	gtggcatcgg	ggctgttctg	caagtgtgaa	cggagacgct	gcctccggat	780
tgtggaaaag	agccgaggg	gtggagtatg	ccggggctgt	cagaccaag	aggattgtgg	840
ccattgcccc	atctgccttc	gccctccccg	ccctggcttc	aggcgccagt	ggaaatgtgt	900
ccagcgacct	tgccctacgg	gtaaacatgc	ccgcccgaag	ggaggctgtg	actccaagat	960
ggctgccagg	cgccgcctcc	gagcccagcc	actgcctcca	ccacccccat	cacagtcccc	1020
agagcccaca	gagccgcacc	ccagagccct	ggccccctcg	ccacctgccg	agttcatcta	1080
ttactgtgta	gacgaggacg	agctacagcc	ctacacgaac	cgccggcaga	accgcaagtg	1140
cggggcctgt	gcagcctgcc	tacggcggat	ggactgtggc	cgctgcgact	tctgtgcga	1200
caagcccaaa	ttcgggggca	gcaaccagaa	gcgccagaag	tgctgttggc	gccaatgcct	1260
gcagtttgcc	atgaagcggc	tgctgcccag	tgtctgggtc	gagctctgag	atggggcagg	1320
atcgccccca	ccttaccgtc	gtcgaaagag	gcccagctct	gcccagcggc	accatcttgg	1380
ccctaccttg	aagcccacct	tggctacacg	cacagcccaa	ccagaccata	cccaggctcc	1440
aacgaagcag	gaagcagggt	gtggctttgt	gctgcccccg	cctggcactg	acctgtgtgt	1500
tttacgggaa	ggcgcaagca	gtcctgtgca	ggtgcccggc	cctgttgcag	cttccacaga	1560
agccctgttg	caggtgaagc	aagagaaggc	ggatacccag	gacgagtgga	caccaggcac	1620
agctgtcctg	acttctcccg	tattgggtgc	tggctgccct	agcaaggcag	tagaccagg	1680
cctgccttct	gtgaagcaag	agccacctga	cccagaggag	gacaaggagg	agaacaagga	1740
tgattctgcc	tccaaattgg	ccccagagga	agaggcagga	ggggctggca	caccgtgat	1800
cacggagatt	ttcagcctgg	gtggaacccg	cttccgagat	acagcagtct	ggttgccaag	1860
gtccaaagac	cttaaaaaac	ctggagctag	aaagcagtag	actggaggct	tctacagact	1920
gtaggattca	agtctgcagg	gcaggcactc	gggaagggaa	gatggatgta	aagtgtggga	1980
gaccgaggac	acagtggagc	ccacgagcac	gagctggaac	ccacgaggat	ggcctggaac	2040
ccatgtcagt	ctctcaccac	ctccagcttc	gatgatgtgg	gtgtcctgca	gaagaagctg	2100
gtgccccttc	tcacagagtt	aaatatgcac	ctggcccagg	aattagagaa	gctgaaagga	2160
tgatcctggg	gaagggtgaa	cagctgcagg	cctggct			2197

WO 00/44900

PCT/US00/02237

<210> 68
<211> 2081
<212> DNA
<213> Homo sapiens

<220>
<221> misc-feature
<223> Incyte ID No.: 1685494CB1

<400> 68
gcatacgagcag tccgtgccta agcggcacga ccatcgagcc aaggtcctcc agcgttccta 60
gagcggagaa gaaagcgctc cgaagagcta gagctgacac tcggcgatga gctaagacgc 120
tgtttcagag cgtttgggtc ctctgaggcc ccttgaccag gagtgtctct gaagatacag 180
tccaaagaag gttctccaaa acaaggagag cagtctgaag ctggggatgg caacagcatt 240
ggtgagtgcc cattccctgg ctccctctgag tctgaagaag gaggggcttc gggtagtgag 300
ggaggatcac tactctactt gggaacaggg attcaagctg caaggaaaca gtaaaggcct 360
tggacaggag ccattgtgca aacaattcag gcagttgctg tatgaagaga ccacaggacc 420
tcgagaagca ctaagtcggc tccgggagct ctgtcaacag tggctacagc ccgagacca 480
taccaaggag cagatcctgg agctgctggt gctggagcag tttctgatca tcctgcctaa 540
ggagctccag gcccgggtgc aggagcatca cccagagagc agggaggacg tggttgttgt 600
tctggaggat ttgcagctgg atcttgagga aacaggacaa cagggtggacc cagaccagcc 660
aaagaacaaa aaaatacttg tggaggagat ggccccctctg aaaggagtag aggaacagca 720
ggttcggcat gagtgtgaag ttacaaagcg tgagaaagag aagggtgagg agacaaggat 780
tgagaatggg aagcttattg tagtaacaga ctcttgagg agagtagagt catctgggaa 840
aatatctgaa cccatggagg ctcataatga gggctctaac ttggaaaggc atcaggccaa 900
gcccacagag aagattgagt ataaatgctc agaacgtgag cagagattca tccagcactt 960
ggacctgatt gaacatgcga gtacacacac gggaaagaaa ctctgcgagt ctgatgtgtg 1020
tcagagttcc agtcttacag gacataagaa agtccctctc agagagaaaag gtcatcagtg 1080
tcagagtgtt gggaaagcct ttcagaggag ttcacacctc gtcagacatc agaaaatcca 1140
tcttggtgag aagccttacc agtgcaatga gtgtggcaaa gtcttttagc agaatgcagg 1200
ccttttgga catctcagaa ttcatactgg agagaaacct tatctatgta tccattgttg 1260
aaaaatttt aggcgcagct ctccacctaa tgcacatcag agaattcaca gtcaggagga 1320
gcctgtgag tgcaaggagt gtggaaaaac ctttagtcag gccttactcc tcaccacca 1380
tcagagaatc catagtcact ccaaaaagcca tcaatgtaac gagtgtggaa aagctttcag 1440
tttgacctca gaccttatc gacaccacag aattcact ggcagaaac ctttcaagtg 1500
taacatatgc cagaaagcct tccgactaaa ctccacctt gtcagcatg taagaatcca 1560
caatgaagaa aaacctatc agtgtagtga atgtggagaa gccttcaggc aaaggtcagg 1620
tctttttcaa catcagagat atcaccacaa agacaaactg gcttgatgag gtgttctctc 1680
cttgtagaac atcagagaag gcacattgac tagcaaacag cacttttaga aaagtcaccg 1740
tagccactg tggcatcaga aaattcttgg gggctgagtt ggaggctccc tgctctatt 1800
ctctctctt tgccttctt gaagtcagct ttggaccaca ataatttcac tgtagatgat 1860
atgctaggat caaagttaaa cagcattctt cactgcagga catctcagag catgtaacat 1920
aactgcatga ttatatactc taagcaatag agagcttcat gactgagtaa gacttttgaa 1980
gtcagcagtg aatcaagtgc ccacagattt gcaggtctaa gcagaacaag ggaagattga 2040
tatttttggg tatgctatag cagctttctc ctatgaaata a 2081

<210> 69
<211> 2785
<212> DNA
<213> Homo sapiens

<220>
<221> misc-feature
<223> Incyte ID No.: 1730829CB1

<400> 69
gaccgtgagg cgcccagcgg agtagggggt gcgcttgggg tttgctgaag ctggctgcct 60
ctccactcc ccttttgggt gcaaagcgcc gctagcggga agacgggggc cgggaggggga 120
caggggcacc tgcgtactgg actgagagcc tgcgcccagc ttacatcgac cccaccgggc 180
cccggcccga cccgacgcga cccgatccga tccgatccca ttccatccgt tctcgtctc 240
ctcccggtct gaccggttgc ccggcggtgg ttcgccacac caggcatcca aagctgagg 300

WO 00/44900

PCT/US00/02237

```

cgctcctacg gectgggctc gccttcgctt tagagatggt tggcctcttc cctcccaaac 360
agctcatctt caaaacctgg actcttggac tggcacctgg ccacctttcc ctctaccaag 420
actccacttc cgtcttacct acttcttctt cagattcttg gtaccccttg ggttggagac 480
tgctcatttt ccttccaaat taatcccaga cccctaaaaa tattgacaac cttgacaacc 540
ccccaaaccga ggagccagac tttgttttgg actaacttcc atagccctat catggaggca 600
gtgtacctgg tagtgaatgg gttgggcttg gtgctggacg tgetgacctt ggtgttggac 660
ctcaacttcc tgetggtgtc ctccctcctg gcttcccttg cctggctcct ggccttcgtc 720
tacaacctgc cgcacacggg actgactagt cttctgcact tgggcccggg agtcttgcct 780
tcattgctgg ccttgatcga agccgtgggc cgggtcacat gtgggggctt gcaggccttg 840
tgtactctgc tgtatagctg ctgctctggc ctagagagcc taaagctcct ggggcacctg 900
gcctctcatg gggcactgag gagcaggagg atactgcacc ggggogtctt caatgtggtc 960
tccagtggcc atgctttgct gcgccaggcc tgtgacatct gtgccattgc catgagcctg 1020
gtggcttatg tgatcaacag cctggtcaac atctgectca tcggcactca gaacctcttt 1080
tccttgggtg tggccctgtg ggtatgcagt accgggcttc tgtggaggat gacagacgta 1140
gtggctgcct tcctagccca catttccagc agtctgttgg ccatggccat cctccttttg 1200
acacctgccc aactagccct ggagctgctg gcctcagctg cccgctcctt ggccagcttt 1260
gtgcttgtca atctcactgg cttggtgttg ctagcttgtg tgetggcagt gacggtgact 1320
gtgttgcatc cggacttcac cctgaggctg gctaccagg cactcagcca gctccatgcc 1380
cggccatctc accaccgtct tcgagaggat gtcctgcggc tctctcgctt agcactgggc 1440
tcagaggcct ggcccgaggt ctggagccgc agtctgcagc tggcgagttg gccaaaccgg 1500
ggagggggcac ctggagctcc ccagggtgac cctatgaggg tattctcagt taggaccggg 1560
agacaggaca ctcttcctga agcggggcgc agatcagagg cagaagagga ggaggccagg 1620
accatcagag tgacacctgt cagggggccga gagaggctca atgaggagga gcctccaggt 1680
gggcaagacc cttggaaatt gctgaaggag caagaggagc ggaagaagtg tgtcatctgc 1740
caggaccaga gcaagacagt gttgtctctg ccctgcgggc atctgtgcct gtgccaggcc 1800
tgactgaaa tctgatgag ccaccccgct taccaccgca attgcccgt ctgccggcgg 1860
ggcatcctgc agaccctcaa tgtctacctc tgaagcctcc tccctgcct gccacccct 1920
ccatgctcca cgcaggcact cagcctagga cagcattaac acctcatctc cgggtcctgg 1980
tctgaatccc ctctacccc tgtggccatc ctgccataca tccaggacat tgagttggaa 2040
gactatgatc tgggtggggg caggataaca tggcttctct ttaccagtg ggtcccttcg 2100
atgctgaggg tgggtgagat gtcactatgc aagggccctg agactatttg ctgtgggctc 2160
tcctccagcc tgcccagggc ccaccagat gcctctgggg ttaccctgt ctgctcttg 2220
tttttctgtt ggagatctat aggtcctttt cctgcctcct tcacatttcc tcccagctt 2280
ttgcggccac aacacatcag tgtcatttgg gtgttttggc aactcagggg ccttcggatg 2340
atcttaaacc tttgtgttca gccagagccc ctgtgccctg gtaggcgttg gggttagtat 2400
ctctcgggtg cctcagagc cacctctgcc tgtgatectg tgatagggt ccctcccaac 2460
ctgatccaaa agccagtctc aggagtttac ccctgggatg ggggatgcat ctgcacctga 2520
ctttggggcc acgtgccttg tggcacccca gctcactggg atctcagga gggataaccg 2580
gatttctgct ctttcccctg tcactccacg atcacacaga aaaatggcat tctctctgt 2640
ctctccctgg catggagagg gcagactgtg cacatttcac tagggttcaa atacagaagg 2700
cccagggccc aggggttgca gcttcgtgag ggtctcttg ccagtttcc aatgaataaa 2760
gttctcttga cagctaaaaa aaaaa 2785

```

<210> 70

<211> 1231

<212> DNA

<213> Homo sapiens

<220>

<221> misc-feature

<223> Incyte ID No.: 1864641CB1

<400> 70

```

tcccgctcta tgacgtcagc cgtaaggcgc tgctgtcgta aaaggacgtc cggctccgtct 60
cctagtgtcc ggaatcggct gtcagcctcc ctggctgtta gtaccttctt tcccgagtc 120
ctggctccacg agttggattt actgctgtcg cgggtgggccc tcacgccatt cctgtccct 180
cggcccccctg agtgagtcgg gtctcccggc gaaagtgagc gaggtttgcc cggagccgct 240
acgaggggaa aatgcctaaa aaaaagactg gtgcgaggaa gaaggctgag aaccgccgag 300
aacgtgaaaa acaactaaga gcatcaagaa gcactataga tttagctaaa catccatgta 360
atgcctcaat ggaatgtgac aagtgtcaga ggccggcagaa gaatagagca ttttgctact 420

```

WO 00/44900

PCT/US00/02237

```

tttgtaatc tgtacagaag ttaccaatct gtgcacagtg tgggaaaaca aagtgcata 480
tgaagtcttc agactgtgtc ataaagcatg ctggtgtata cagtactggc cttgcaatgg 540
tgggtgcaat atgtgacttc tgtgaagctt gggtttgcca tggtaggaaa tgtctcagta 600
cacatgcttg tgccctgcct cttaccgatg ctgagtggtg tgaatgtgaa cgaggcgtgt 660
gggaccatgg aggcagaata ttcagttgtt ctttttgcca taactttctc tgtgaagatg 720
atcaatttga gcatcaagcc agctgccagg ttttagaggc agaaacattt aaatgtgttt 780
catgcaatcg gcttgggtcag cactcatgtc tccgttgtaa ggcttgtttc tgtgatgatc 840
atacaaggag caaagtgttt aagcaagaaa aaggaaaaca gcctccttgt cctaaatgtg 900
ggcatgaaac tcaggagact aaggacctta gcatgtcaac acgctccctg aaatttgga 960
ggcagactgg aggtgaagag ggagatggag cttctgggta tgatgcttat tgggaagaacc 1020
tttcatctga taagtatggg gataccagct accacgatga ggaggaggat gagtatgaag 1080
cagaggatga tgaagaggaa gaagatgaag gcagaaagga ttcagatact gagtcatcag 1140
atttgtttac taatttgaat ttaggaagga cctatgctag tggctatgct cactatgagg 1200
aacaagagaa ctaggggagc tgctctgggtg g 1231

```

```

<210> 71
<211> 700
<212> DNA
<213> Homo sapiens

<220> -
<221> misc-feature
<223> Incyte ID No.: 2444604CB1

```

```

<400> 71
gccccagggtg acacaatggc cgcagtcctat ggccggctggc ttcttccage ccttcatgtc 60
accgcgcttc ccagggggcc cccggcccac cctgcggatg ccgagtcagc ctcccgcata 120
cctccctggc tcccagcccc tcctccctgg cgccatggag cctccccac gagccaggg 180
gcatccgagc atgggcccgc caatgcagag ggtgacgctt cctcgtggca tggccagcgt 240
ggggcccccag agctatggag gtggcatgctg acccccaccc aactccctcg ccggcccagg 300
cctgcctgcc atgaacatgg gccaggaggt tcgtggcccg tgggcccagc ccagtggaaa 360
ctcgatcccc tactcctct catccccgg cagctacacc ggacccccag gaggagggtg 420
gccccctgga acacccatca tgccatagccc tggagattcc accaactcca gcgaaaacat 480
gtacactatc atgaacccca tcgggcaggg cgccggcagg gctaatttcc cgctcggccc 540
tggcccgagg ggcccatggc cgccatgagc gcatggagc ctcaccacgt gaacggatcc 600
ctgggctcgg gcgacatgga cgggttgccg aagagttccc ccggcgccgt ggccggcctg 660
agcaacgccc cggggcaccc cgcgggacga cggcgagatg 700

```

```

<210> 72
<211> 2332
<212> DNA
<213> Homo sapiens

<220>
<221> misc-feature
<223> Incyte ID No.: 2445008CB1

```

```

<400> 72
aggcggacgg ggaacgagge cgtcggccat tttgtgtctg ctctctgtgg gacgtggtgg 60
tagccgttgg gttgggaaag tgagggattt ttggcctcgt ttctctgtct tcttttctcc 120
tcccttttac tttgccggtg gaacacagtt atgggtcgca agaagaagaa gcagctgaag 180
ccgtggtgct ggtattgtaa tagagatttt gatgatgaga agatccttat tcagcaccac 240
aaagcaaagc attttaaatg ccataatgtt cacaagaaat tgtatacagg acctggctta 300
gctattcatt gcatgcaggt acataaagaa acaatagatg ccgtaccaa tgcaatacct 360
ggaagaacag acatagagtt ggaaatatat ggtatggaag gtattccaga aaaagacatg 420
gatgaaagac gacgacttct tgaacagaaa acacaagaaa gtcaaaaaaa gaagcaacaa 480
gatgattctg atgaatatga tgatgacgac tctgcagcct caacttcatt tcagccacag 540
cctgttcaac ctgagcaagg ttatattcct ccaatggcac agccaggact gccaccagta 600
ccaggagcac caggaatgcc tccaggcata cctccattaa tgccagggtg tctcctctctg 660
atgccaggaa tgccaccagt tatgccaggc atgccacctg gattgcatca tcagagaaaa 720

```

WO 00/44900

PCT/US00/02237

```

tacacccagt cattttgctg tgaaaacata atgatgccaa tgggtggaat gatgccacct 780
ggaccaggaa taccacctct gatgcctgga atgccaccag gtatgcccc acctgttcca 840
cgctctggaa ttcttccaat gactcaagca caggctgttt cagcgccagg tattcttaat 900
agaccacctg caccaacagc aactgtacct gcccacagc ctccagttac taagcctctt 960
ttccccagtg ctggacagat ggggacacct gtcacaagct caagtacagc ttcatccaat 1020
tcagaaagtc tgtctgcac ttctaaagct ctgtttctta gcacagcaca agctcaggca 1080
gctgtccaag gacctgttgg tacagatttc aaacctttaa atagtacccc tgcaacaact 1140
acagaacccc caaagcctac attccttctg tatacacagt ctacagcttc aacaactagt 1200
acaacaaata gtactgcagc taaaccagcg gcttcaataa caagtaagcc tgctacactt 1260
acaacaacta gtgcaaccag taagttgac catccagatg aggatataat cctggaagag 1320
agaagggcac agttacctaa gtatcaacgt aatcttcttc ggccaggaca ggcccccttc 1380
ggtaatccac cagttggacc aattggagggt atgatgccac cacagccagg catcccacag 1440
caacaaggaa tgagaccccc aatgccacct catggctcagt atgggtggtca tcatcaaggc 1500
atgccaggat accttctctg tgcctatgcc ccgtatgggc agggaccgcc aatggtgcc 1560
ccttaccagg gtgggctctc tgcacctccg atgggaatga gacctcctgt aatgtcgcaa 1620
gggtggcctt actgatctta ctctatccag tctaataagg ttggagatta aaccttttct 1680
caacttctgc tgtttatata gccaaagcttc cgtcaataag gcttcattgt gactttaaca 1740
aacattatct tcccacatac caggaaactat tggacattta ttttacatgg gaaaaattat 1800
ttggaataat aaagcaggaa ctttctctga agttgcaatt tatactgtat ggcttctttt 1860
tcatgtttca tctaggtttt tagaagttaa gtatagtaaa tttggttcgt taaattgtga 1920
agggcgtgga attacatgaa cataccaccc tagtaaaggc aagttctgta agcttacatt 1980
gctatttcta aagtttgcct tcacagcatt tcagatgctg ttggacttca tgtccccaac 2040
ctagcttggg gagggctgta actgtttcca agtacttgta cattggaagt ctgaatgtgt 2100
aacaattatt aatgtattta gacttctcca tgttgcagg ttttaagaaat ctgacccacc 2160
aaggtcatgt gacttttctg tactgttaaa ctctattgta ataaaatgag agaaaaattt 2220
atgccttttt attcataacc cagctgtgga ccactgcctg aaaggtttgt acagatgcat 2280
gccacagtag atgtccacat aataaaattc atagttacca aaaaaaaaaa aa 2332

```

<210> 73

<211> 1936

<212> DNA

<213> Homo sapiens

<220>

<221> misc-feature

<223> Incyte ID No.: 2572462CB1

<400> 73

```

ttggttctat attactgttt tatagctgag gagaaagact cacatcattt actaagatca 60
tatagctagc tagtaaatgt ttgagtgaat atacaaacaa aggttttctg actttaagag 120
cttgagtttt ttccactata ccataattgca tctgttgtaa ttggttaacta atgtgcattt 180
taaaattctc atttgtctta tgtactgagc ccttatacca gtgctaattt atgtgactcc 240
tttctcctgc agctaagaga aaaatacctt ttaattcat ttatagtacc cagtttttaa 300
agaagattta ttttgtaaaa ttttgcttat ggtacatgtc atcttagcct gtaaataaat 360
taaagcatta atttttatcc ctccctgggc ttttctctct tctgacttta tacgtcttcc 420
tagagagctt atcttctata ataacaattc tttgttttaa agtgagaaaag atcagtctaa 480
agaaaaggag aagaaagtga aaaaaacaa tcttctctgg gctacccttt ctgccagcca 540
gctagccagg gccagaaaac aaacaccgat ggcttcttcc ccacgtacca agatggatgc 600
aatcttaact gaggccatta aggcattgct ccagaagagt ggtgcacacg tgggtgctat 660
tcgaaaatac atcatccata agtatccttc tctggagctg gagagaaggg gttatctcct 720
taaacaagca ctgaaaagag aattaaatag aggagtcac aaacagggtt aaggaaaagg 780
tgcttctgga agttttgttg tgggttcaga atcaagaaaa acacctcaga aatccagaaa 840
cagaaagaat agggagctct cagtggatcc agaaccacaa gtaaaattgg aggatgtcct 900
cccactggcc tttactcgcc tttgtgaacc taaagaagct tcctacagtc tcatcaggaa 960
atatgtgtct cagtattatc ctaagcttag agtggacac aggcctcagc tgttgaagaa 1020
cgctctgcag agagcagtag agaggggcca gttagaacag ataactggca aagggtgctt 1080
ggggacattc cagctgaaga aatcagggga gaaacccctg cttggtggaa gctgatgga 1140
atatgcaatc ttgtctgcca ttgtctccat gaatgagccg aagacctgct ctaccactgc 1200
tctgaagaag tatgtcttag agaatcacc aggaaccaat tctaactatc aatgcatatt 1260
gctgaaaaaa accctgcaga aatgcgaaaa gaatgggtgg atggaacaga tctctgggaa 1320
aggggttcagt ggcaccttcc agctctgttt tccctattat cccagcccag gagttctgtt 1380

```

WO 00/44900

PCT/US00/02237

```

tccgaagaaa gagccagatg attctagaga tgaggatgaa gatgaagatg agtcatcaga 1440
agaagactct gaggatgaag agccgccacc taagagaagg ttgcagaaga aaaccccagc 1500
caagtcccca gggaaggccg catctgtgaa gcagagaggg tccaaacctg cacctaaagt 1560
ctcagctgcc cagcggggga aagctaggcc cttgcctaag aaagcacctc ctaaggccaa 1620
aacgcctgcc aagaagacca gaccctcatc cacagtcata aagaaacctc gtggtgggtc 1680
ctcaaagaag cctgcaacca gtgcaagaaa ggaagtaaaa ttgccgggca aggggcaaatc 1740
caccatgaag aagtctttca gagtgaaaaa gttaaatttta taggaaaaaa gggatatcatg 1800
atgaaattca aaatcttatt ttctaaggtc agtgtgcatt tgtttagttt tgatgctttt 1860
caaattacat tattttcttc ccctatgaac attgtgggga gggactctaa ataaaccagt 1920
ttaggcaaaa aaaaaa
1936

```

<210> 74
 <211> 1667
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc-feature
 <223> Incyte ID No.: 2572892CB1

```

<400> 74
cgcgaaatcgg cgaccccagt gacctgacca ctatgccgcg ctctttcttc gtcaggaagc 60
cctccgaccc caatcggaag cctaactaca gcgagctgca ggactctaat ccagagttta 120
ccttccagca gccctacgac caggccacc tgctggcagc catccacct ccggagatcc 180
tcaacccac cgctctgctg ccaatgtctc tctgggactc tgtcctggcg ccccaagccc 240
agccaattgc ctgggctctc cttcggtctc aggagagtcc cagggtggca gagctgacct 300
ccctgtcaga cgaggacagt gggaaaggct cccagccccc cagccacccc tcaccggctc 360
cttcgtcctt ctctctact tcagctctt ccttgaggc cgaggcctat gctgccttc 420
caggcttggg ccaagtgcct aagcagctgg cccagctctc tgaggccaag gatctccagg 480
ctcgaaaggc cttcaactgc aaatactgca acaaggaata cctcagcctg ggtgccctca 540
agatgcacat ccgaagccac acgctgccct gcgtctgcgg aacctgcggg aaggccttct 600
ctaggccctg gctgctacaa ggccatgtcc ggacccacac tggcgagaag cccttctctc 660
gtccccactg cagcctgtgc ttcgctgacc gctccaaact gcgggccac ctccagaccc 720
actcagatgt caagaagtac cagtgcagg cgtgtgctcg gaccttctcc cgaatgtccc 780
tgctccacaa gcaccaagag tccggctgct caggatgtcc ccgctgaccc tcgaggctcc 840
ctcttctctt ccatacctgc ccttgcctga cagccttccc cagctccagc aggaaggacc 900
ccacatcctt ctcaactgca tggaaattccc tcttgagtgc cccacttctg gccacatcag 960
ccccacagga ctttgatgaa gaccatttcc tggttctgtg tctctgctt gggctctgga 1020
agaggccttc ccgtggccat ttctgtggag ggagggcagc tggcccccag ccctggggga 1080
ttcctgagct ggctgtctg cgtgggtttt tgtatccaga gctgtttgga tacagctgct 1140
ttgagctaca ggacaaaggc tgacagactc actgggaagc tcccacccca ctccaggggac 1200
cccactcccc tcacacacac cccccacaa ggaacctca ggccacctc caccaggtgt 1260
gactaactat gcaataatcc acccccagg gcagcccccag ggctgcgga ggcggtggca 1320
gactagagtc tgagatgccc cgagcccagg cagctatttc agcctcctgt ttggtggggt 1380
ggcacctgtt tcccgggcaa ttaacaatg tctgaaaagg gactgtgagt aatggctgtc 1440
acttgtcggg ggcccaagtg ggggtgctct gtctgaccga tgtgtctccc agaactatc 1500
tgggggcccc acaggtgggc ctgggaggaa gatgtttaca tttttaagg tacactggta 1560
tttatatttc aaacattttg tatcaaggaa acgttttcta tagttatatg tacagtttat 1620
tgatattcaa taaagcagtt aatttatata ttaaaaaaaaa aaaaaa 1667

```

<210> 75
 <211> 759
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc-feature
 <223> Incyte ID No.: 2785674CB1

<400> 75

```

tgggctcgcc tccctgggac taggtttcag cggcgcgtgc gatgaccaa ataaaggcag 60
atccccgacgg gccccaggct caggcggagg cgtgttccgg ggagcgcacc taccaggagc 120
tgctgggtcaa ccagaacccc atcgcgcagc ccttggttcc tgcgcgcctc acgcggaagc 180
tctacaaatg catcaagaaa gcggtgaagc agaagcagat tcggcgcggg gtgaaagagg 240
ttcagaaatt tgtcaacaaa ggagaaaaag ggatcatggg tttggcagga gacacactgc 300
ccattgaggt atactgccat ctcccagtc tgtgtgagga ccgaaatttg ccctatgtct 360
atatccccctc taagacggac ctgggtgcag ccgcaggctc caagcgcccc acctgtgtga 420
taatgggtcaa gccccatgag gagtaccagg aggtttacga tgagtgcctg gaggagggtgc 480
agtccctgcc cctaccctca tgaggggctc cggtagcacc tgggcacctg ccgctggaag 540
ctattgggct ggcagcagga cgactggctg tcttctgccc caccacact gacggcatct 600
tcccagttcc ccaaggcacg ccttcttccc aggcagctct aacagccctt tcatgaaggt 660
aatgctagtc ttctgtccat cagtgccatt tctgtagaa ctaaaggctg ttccaagaat 720
gtgggggtggg gaaagtaaat gctaagacta aaaaaaaaa 759

```

<210> 76
 <211> 1421
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc-feature
 <223> Incyte ID No.: 2797479CB1

```

<400> 76
ccccagtcac tgttctctgcc cgttgccctgt cagcctcact gcctttaate cgcttccagg 60
gctcattcac ctgaatatat tggttgccat gtcgagatat ggtgaggata ctgcgcaagg 120
catccccgat ccgaaccttc tcaagtagct gttgatatag ctggagctcc acggtgacat 180
gagctaacag gcgctgatca tcatgggtga tgacatatcg acgcacatag ccccaaaaga 240
acttagacac aaacatccca gctctgttga tgaagttgcc caggttggtta agcagctcag 300
aattattctt cagcagcagg tccgtccagg agaaagcact gtccctggccc tcaggccgaa 360
tgtacagcag atagaagcgc cagatgtcag cagggatccc cgtgtcctgg gctttgattt 420
tcttgggttca gcacgaattc atgaaggaa cccactctca gagaaacct atgaatgtaa 480
gcaatgtggg aaattgttat ctcatcgctc aagctttcga agacacatga tggcacacac 540
tggagatggc cctcataaat gcacagtatg tgggaaagcc tttgactctc ctagtgtatt 600
tcaaagacat gaaaggactc aactgggaga gaaacctat gaatgcaagc aatgtgggaa 660
agccttccgt acttccagtt ccttccgaaa acatgaaaca acacacactg gagagcaacc 720
ctataaatgt aaatgtggaa aagcttttag tgatttattt tcttttcaaa gtcataaaac 780
aacacacagt gaagaggagc cttatgaatg taaggagtgt gggaaagcat ttagttcttt 840
taaatacttt tgcgccatg aacggactca cagtgaagaa aaatcttatg agtgtcaaat 900
ttgtggcaaa ctttcagtcg tttcagttac ttaaaaactc atgaaaggac tcacacggca 960
gagaagccat atgaatgtaa gcaatgcagg aaagcattct tttggccctc tttccttcta 1020
agacatgaaa ggactcacac tggagaaaga cctatgaat gtaaacactg tggtaaagcc 1080
ttcagtcggt ccagtttctg tcgagaacat gaaagaactc acgctggaga gaagccctat 1140
gaatgtaagg aatgtgggaa agccttcagt tctctcagtt cctttaatag acataaaaagg 1200
acacactgga aggatattct ataagtgtat ggaatgtggg aaagcattca ttgggttttat 1260
cacattcaga tacttgaaag aaataaatcc tgtgaatgta aacgtggtaa agccttaaga 1320
agtttccagg ctgggcgcag cggtccacac agcactttga gaggccgagg 1380
agggcataatc acgaggccag gagatcgaga ccagcctggg g 1421

```

<210> 77
 <211> 2386
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc-feature
 <223> Incyte ID No.: 2960640CB1

```

<400> 77
gacttttaag ggatcacaga gctcacacca aagaccaggg gaacagtcag aagcctggct 60

```

WO 00/44900

PCT/US00/02237

tgtctctcag	gtctccagga	acctgcctca	aaacacaggt	ctccacgacc	aggagacagg	120
tgctgtggtc	tggaacagctg	ggtcccaggg	accagccatg	cgtgacaaca	gagctgtatc	180
cctctgtcag	caagaatgga	tgtgcccagg	ccctgcacaa	agggccctct	acaggggtgc	240
caccagagg	aaggacagtc	acgtctcgt	ggcaacaggt	gtgccctggg	gctatgaaga	300
gaccaagacg	ctcctggcta	ttcttagtag	ttctcaattt	tatggaaaac	tccagacctg	360
tcagcagaac	agccagatct	acagggccat	ggcggaaagga	ctctggggagc	aggggtttct	420
gcggaaccca	gaacagtgtc	gcaccaagtt	caaaagccta	cagtttgagtt	accgcaaagt	480
gaggagaggc	cgtgtgcctg	agccttgtat	cttttatgag	gaaatgaatg	ctctttcagg	540
ctcctgggccc	tctgcacctc	ctatggcaag	cgatgctgtt	cctggccaag	aaggaaagtg	600
tattgaggct	ggagagctga	atcaccagaa	tggggaaccc	acggaggtag	aagatggcac	660
tgtggatggt	gcagacaggg	atgaaaagga	cttcaggaat	cctggccagg	aagtcaggaa	720
actagacctg	ccagtgtctg	tcccaaacag	acttggtttt	gagttcaaga	acgagattaa	780
aaaagaaaaat	ctaaaatggg	atgattcaga	ggaaagtagaa	ataaacaagg	ctttacagag	840
aaagtccaga	ggagttttat	ggcactctga	gctacaaaaa	ggcttggaga	gtgagccaac	900
atcaagaagg	caatgtagaa	attctccagg	ggagagttag	gagaaaaccc	catcccagga	960
gaagatgagt	caccagagtt	tttgtgccag	ggacaaaagcc	tgtacacata	tctctgtgtg	1020
gaaaaactgc	tctcagagt	tgcactctcc	ccacaagcca	gcgctcaaac	tggaaaaagt	1080
atctcaatgt	cctgaatgtg	ggaaaacctt	tagccgaagt	tcttatcttg	ttcggcatca	1140
aagaatccac	acagggcaga	agcctcacaa	gtgcagttag	tgcgggaagg	gctttagtga	1200
gcgctccaac	ctcactgccc	acctacgaac	tcacacaggg	gagaggccct	atcagtgtgtg	1260
gcaatgtggg	aaaagcttca	accagagttc	cagcctcatt	gtccaccaga	ggacccatac	1320
cggggaaaaag	ccttaccagt	gcattgtctg	tggaaaagaga	ttcaacaaca	gttcccagtt	1380
cagtgtcac	cggcgcatcc	acactgggga	gagcccatat	aagtgtgcag	tgtgtgggaa	1440
aatcttcaac	aatagctccc	acttcagtgc	ccaccgaaaa	accacactg	gtgaaaagcc	1500
ttacaggtgt	tctcactgtg	agagaggctt	cactaagaac	tctgcccctca	cccgatcatca	1560
gacagtacac	atgaaagcag	tactctcatc	acaggaagga	agagatgcgt	tatgagtgtg	1620
toggtaaact	gtcagattaa	gttccctcagg	tcagcatgta	tgagctttct	tctgctgtgtg	1680
agagatctag	ccagtccctg	actttgcaac	agacctactg	actactggat	cttaagacct	1740
atgtctagga	ccaggagtca	gcataaggac	gctgacctct	cctggctgtg	cctgtgactc	1800
cagagtcccta	tcttactgtg	acttaaagtt	tgatggagag	aaagctgtag	gatccataaa	1860
ttctaccagg	aatccagggg	cttctgtttc	ctagcactga	gaatgggcac	ccagtgggtcc	1920
aagaacactt	tctgggctaa	catagtctct	acacaggggt	gagaaagaaa	gtgtctcctt	1980
tcttggaag	cacatgtaaa	agttaaaggg	ctgaatctct	tctaaaccaa	taattgacct	2040
ctaggcaccc	accgtaatac	tgctaccttc	atgacagaag	acactgctct	ttgtaaccca	2100
gccaccacca	aaaagcaaac	agaaagaagg	aaggatgggt	aagccatttg	ataatactga	2160
atctgtttcc	ctaagtgact	taaccttaga	gcaagcaca	catccaggtt	aattaattgt	2220
aagattttct	ctctcattat	tgcctcatc	atagttcctg	attgtctctt	aaagtaagt	2280
gtttatagac	attactatct	ctgataataa	tttacaaact	actataaaca	aattttataa	2340
cattactaat	ttctgatgaa	aataaagttg	tttctccctc	caccac		2386

<210> 78
 <211> 1432
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc-feature
 <223> Incyte ID No.: 3454051CB1

<400> 78						
agtatgagct	ggacctgtcc	gcgttgccag	caacctgttt	tcttcgctga	gaaggtgagc	60
tccctgggca	agaactggca	ccgcttctgc	ctgaaatgtg	agcgctgcca	cagcatcctg	120
tccctgggcg	ggcatgcaga	gcacaatggg	agggcatact	gccacaagcc	atgctatggg	180
gctctctttg	gacccagggg	ccctcccatc	atgaagacat	tcactgggga	gacctcgctg	240
tgccttggtt	gtggggagcc	cgtctatatt	gctgagaagg	tgatgtcatt	aggcagaaat	300
tggcaccgac	cgtgtctgag	gtgccagcgt	tgccacaaga	ccctgactgc	tgggagtcac	360
gctgagcatg	atggagtccc	ctactgccac	gtccccctgt	acggctacct	gtttggcccc	420
aaaggtgtga	acattggcga	tgtgggctgc	tacatctatg	acccagtga	gataaaattc	480
aaatgagacg	ctcacaaaaa	aggtcaccc	aactcaggcc	tcccatcatg	ccctcatggg	540
tccaatggaa	gctacaaaaa	tctccagctc	catgggggtt	ggggaagggt	ggatcttggg	600
ggcctggggc	taggtcccat	ggtaggccag	agagtctaga	ctttctctgc	caattttttc	660

WO 00/44900

PCT/US00/02237

<220>
<221> misc-feature
<223> Incyte ID No.: 3815083CB1

<400> 80
ctcagggtccg gagcgcggtc gggacacagc gcctctagga gaaagcctgg aaggcgctcc 60
gggggtatcc agagctctta gcgggccggc agcatgtgcg gggccccagt aaatggaaat 120
gttttctaac atataaaaaac ctacagaaga agaaaaataat tttctggatc aaattagaag 180
tctgtattat attgatgtct ccagattcaa atatattaga aagcagccgt ggagacaacc 240
atcttcatct tgggagaaat aactaaagcc cgcctcaagc attagaacta cagacaaacc 300
ctgatgagac ctctccagat tgtcccaagt cgattgattt ccagctata ttgtggcctg 360
aagcctccag cgtccacacg aaaccagatt tgcctgaaaa tggctcggcc aagttcaagt 420
atggcagatt ttcgaaagtt ttttgcaaaa gcaaagcaca tagtcatcat ctcaggagct 480
ggtgttagtg cagaaagtgg tgttccgacc ttcagaggag ctggagggtta ttggagaaaa 540
tggcaagccc aggacctggc gactcccttg gcctttgccc acaaccctgc cgggtgtgg 600
gagttctacc actaccggcg ggaggtcatg gggagcaagg agcccaacgc cgggcaccgc 660
gccatagccg agtgtgagac cgggtctggc aagcagggcc ggcgagtcgt ggtcatcacc 720
cagaacatcg atgagctgca ccgcaaggct ggcaccaaga acctctctga gatccatggt 780
agcttattta aaactcgatg tacctcttgt ggagttgtgg ctgagaatta caagagtcca 840
atgtgtccag ctttatcagg aaaaggtgct ccagaacctg gaactcaaga tgccagcatc 900
ccagttgaga aacttccccg gtgtgaagag gcaggctgcg ggggcttgct gcgacctcac 960
gtcgtgtgtg ttggagaaaa cctggatcct gccattcttg aggaggttga cagagagctc 1020
gccactgtg atttatgtct agtgggtggc acttccctct tgggtgacct agcagccatg 1080
tttgccccc aggtggctgc caggggcgtg ccagtggtct aatttaacac ggagaccacc 1140
ccagctacga acagattcag gtttcatttc cagggacct gtggaacgac tcttccctgaa 1200
gcccttgctc gtcatgaaaa tgaaactgtt tcttaagtgt cctggggaag aaagaaatta 1260
cagtatatct aagaactagg ccacacgcag aggagaaatg gtcttatggg tggtagctg 1320
agtactgaac aatctaaaaa tagcctctga ttcctctgct ggaatccaac ctgttgataa 1380
gtgatggggg tttagaagta gcaaagagca cccacattca aaagtcacag aactggaaag 1440
ttaattcata ttatttggtt tgaactgaaa cgtgaggtat ctttgatgtg tatggttggt 1500
tattgggagg gaaaaatttt gtaatttaga ttgtctaaaa aaaataaaaa aaaaaa 1556

<210> 81
<211> 1951
<212> DNA
<213> Homo sapiens

<220>
<221> misc-feature
<223> Incyte ID No.: 3988457CB1

<400> 81
ctccgattat gggataggag aagtgcccggt ggagcccctg gatgtccctt taccctccac 60
gatcaggcca gcttcccccg ttggccgggtc tccaaagcag ccggtgctgt gctactaccg 120
tggcgctgtc ggtggcacgt ttgaccgctt gcacaacgcc cacaagggtg tgctcagtgt 180
cgcgctgcat ctggcccagg agcagcttgt ggtgggagta gcagacaaag atctgttgaa 240
gagcaagttg ctccctgagc tgetccaacc ttatacagaa cgtgtggaac atctgagtga 300
attcctgggtg gacatcaagc cctccttgac ttttgatgtc atccccctgc tggaccctta 360
tgggcccgtt ggtctgacc cctccctgga gtctcctgtg gtcagcgagg agacctatcg 420
tggggggatg gccatcaacc gcttccgctt tgagaatgac ctggaggaaac ttgctttgta 480
ccagatccag ctgctgaagg aactcagaca tacagagaat gaagaggaca aagtcagctc 540
ctccagcttc cgcagcgcaa tgttggggaa cctgcttcgg cctccatatg aaaggccaga 600
gtccccaca tgtctctatg taattgggct gactggcctc agtggctctg ggaagagctc 660
aatagctcag cgactgaagg gcctgggggc gtttgtcatt gacagtgacc acctgggtca 720
tcgggacctat gcccagggtg gccctgccta ccagcctgtg gtggaggcct ttggaacaga 780
tatttccat aaagatggca tcatcaacag gaaggtccta ggcagccggg tgtttgggaa 840
taagaagcag ctgaagatac tcacggacat tatgtggcca attatcgcaa agctggcccg 900
agaggagatg gatcggtctg ttgctgaggg aaagcgtgtg tgtgtgattg atgccgctgt 960
gttgcctttaa gccggtctgc agaacctggt ccagtgaggtg tggactgctg tcatccaga 1020
gactgaggct gtaagacgca ttgtggagag ggtgggctc agtgaagccg cggctcaaag 1080
ccggctgcag agccagatga gcgggcagca gcttgtggaa cagagccacg tgggtgctcag 1140

WO 00/44900

PCT/US00/02237

gatctgtgtt	cacagacatc	tgggggaaga	aaaggagcag	gaaactaccc	cgcacagagt	240
taagcaggaa	acaacaacaa	catcatgcaa	aaaccctgca	aagaaaacga	aggaaagcca	300
aagtgcagcg	tgccaaagag	ggaggaaaaa	cgcccgatat	gagaatttga	acgccagcaa	360
acagaaggga	atcttagaca	gaggctgctt	cagtcctctc	aagaatttaa	agaggacata	420
gactataggc	atcttaaaaga	tgaagaaatg	acaagggagg	gagatgagat	ggaaagggtg	480
ttggaagaga	taaggggtct	gagaaagaaa	tttagggctc	tgcattctaa	ccatagggcat	540
tctcgggacc	gtccttatcc	catttaatta	atttctctga	caattcaatt	atcttctgtt	600
attaatgttg	ccactgcttt	ctgtttgtct	gcactttctt	gataaatatt	tgctatcgtt	660
ttactccagt	cattcgatgt	tgctgagatt	tacatatgac	tcttgtaaac	atctcatctt	720
ttgacccaat	cttattcatt	taataagagg	tctcattcat	ttgcatggaa	aaatgctcat	780
tgtatattgc	aaagtgaaaa	taacgagttg	caaaacagtg	tatacatata	tgtgtgtata	840
tatgtacact	ttatttgtac	atttctatgt	gacataatgc	aaaggaaagt	gtctgatttt	900
attatacacc	aaagggttaac	agtgaatctc	tgtgtgatct	cttttttttt	ctttttgcct	960
atctgcatct	tctcacttgc	caaaaaatga	atatatgttt	atgtgtgtat	attacttgtg	1020
tcacaaaaaa	ccctaaagta	gacagtaaaa	gaacttgtca	atcgcttttg	gaaggcaatg	1080
aaacacttaa	taaactctca	ataacagaag	cgtaaaaatg	aaatgtaaac	ctccaattac	1140
ctctggatct	cttagccaga	gtaataaaact	ggtaattatt	acagataaaa	aaaaaaa	1197

<210> 84

<211> 2170

<212> DNA

<213> Homo sapiens

<220>

<221> misc-feature

<223> Incyte ID No.: 669862CB1

<400> 84

agcgtgcg	ataggacagg	gccttaaatt	catgggttatg	tgtttggttt	tcattctaa	60
ataaagccga	accactgaca	aaattatata	gagagcaatg	tgataatgtt	aggaatagag	120
atattcagga	catactcctg	tgcattctga	tccactcagt	ctgagtggat	atctaaaaga	180
tagtgtatgt	aaaatgtctc	tatggtaatt	ctgatttgca	actaaatatg	agaacttagt	240
actttgtctt	tgctactca	taaatcttac	atcctcctgt	gcactttcat	aattttctgt	300
gcccttcttg	ccttttata	attgcttggc	agtacttttag	aattttctaa	actctttgat	360
tactaacaga	tacacttttt	agttgatcac	tatttttaat	atagatgtcc	tctccctacc	420
cgctattatt	ggaaaatagc	atttgtttgt	tttttcattt	tcttccagac	tttaatttca	480
caactgaaa	caacaagtta	tcttcagaaa	aaagaaatta	tgaagttaaa	gcgtaccatc	540
aggagacatg	gaaaagaaat	aaaaccttca	accttatgag	gtttattttc	agaactgacc	600
cacagtacac	aattgaattt	gggagacaa	agagacctaa	agtgggatgt	tttagtcaaa	660
tgatattcaa	aaaacataaa	tcccttctct	tacataagag	aaataacaca	agagagaaat	720
catatgagtg	taaggaatat	aagaagggct	ttagaaaata	tttgcacctt	actgaacatc	780
tgagagacca	tactggtgtg	ataccctatg	aatgtaatga	atgtggaaaa	gcattttagt	840
ttttccagca	ttttattaga	catcgaaaaa	tccacactga	tttgaaaccc	tatgaatgca	900
atggatgtga	gaaggccttt	agggttttatt	cacagcttat	tcagcatcag	ataattcata	960
ctggtatgaa	accctatgaa	tgtaagcaat	gcgggaaggc	tttttagacgt	cattctcacc	1020
ttacagaaca	tcagaaaatt	catgttggct	tgaaccctt	tgaatgtaag	gaatgtgggg	1080
aaacgttttag	attatatoga	catatgtgtc	gcatacagaa	aattcatcat	ggtgtgaaac	1140
cctacaaatg	taaagaatgt	ggaaaggctt	ttggtcatcg	ttcaagtctt	taccaacata	1200
agaaaattca	ttctggtgag	aaaccatata	aatgtgaaca	atgtgaaaag	gcctttgttc	1260
gcagctatct	acttgttgaa	catcaaagaa	gtcatactgg	tgagaaacct	catgaatgca	1320
tggatgtgg	aaaggctttt	agtaagggtc	caagccttct	taaacataag	agaattcata	1380
gtagtgtgaa	actctatgat	tgtaaggatt	gtggaaaggc	cttttgtaga	ggctctcaac	1440
ttacacagca	tcagagaatt	catactgggtg	agaagccaca	tgaatgtaaa	gaatgtggga	1500
agacttttaa	gcttcattca	tatcttattc	aacatcagat	aattcatact	gatttgaagc	1560
catatgaatg	taagcaatgt	gggaaagcct	tcagtcgtgt	tgagacactt	aagacacatc	1620
aatcaattca	tgctggggag	aaaccctatg	aatgtaagga	atgtggaaaa	accttttagac	1680
ttaattctca	actaatttat	catcagacaa	ttcatactgg	tttgaaaccc	tatgtatgta	1740
aagaatgtaa	gaaggccttt	cgttctatct	caggctcttc	tcaacataag	agaattcata	1800
ctggtgaaaa	accctatgaa	tgtaagaagt	gtgataaggc	ctttaatcgc	agtgatcgac	1860
ttactcaaca	tgagacaatt	catactgggtg	tgaaccacaa	gaaatgcaaa	gaatgtggta	1920
aggccttttag	tcattgctat	caacttagtc	aacatcaaa	atttcacat	ggtgagagac	1980

WO 00/44900

PCT/US00/02237

```

gaaggggtgg gctttgcgaa gatggcgggc ctgggggtgc tggagtcga cctgccaagt 180
gccgtgacac ttctgaaaaa tctccaggag caagtgatgg ctgtaactgc acaagtgaaa 240
tactgacac aaaaagttca agctggtgcc tatcctacag aaaaggtct cagcttcttg 300
gaagtgaag accagctgct gctcatgtac cttatggatt tgaccacct cattctggac 360
aaagcctcag gaggatctct tcaggacat gatgcagttt tgagactggg agagattcga 420
acggttttgg aaaagcttcg tcccttggac caaaagctga agtatcaaat tgacaagctg 480
atcaagactg cagtgcaggg cagccttagt gagaatgacc cacttcgttt taagcctcat 540
cccagcaata tgatgagcaa gttgagctct gaggatgagg aggaagatga agcagaagat 600
gaccagtctg aggccttcagg gaagaaatct gtgaaggagg tgtctaagaa atatgttctt 660
ccacgcttgg ttccagtaca ttatgatgaa acagaagctg agcgggagaa gaagcgtcta 720
gaacgagcca agagacgggc attgagcagc tctgtcattc gtgaacttaa ggagcagtac 780
tcagatgctc cagaggaaat ccgtgatgct cggcatcccc atgttaccct ccagagtcag 840
gaggaccaac acaggattaa ctatgaggag agcatgatgg tgcgtttgag cgtcagtaag 900
cgagagaaag gacggcgaaa acgagcaaat gtcatgagct cacaacttca ttcccttaca 960
cacttcagtg acatcagtcg tttgacaggg ggaactgttc atcttgatga ggatcagaat 1020
cctattaaga agcgggaagaa gatacctcag aaaggtcggg agaaaaaagg ttttcggagg 1080
cggcggtgat tatgggtgta catatttgta tttttttgt catcctgaga tacttcta 1140
ttcattgtat ataggtggtt ttccctggaa ttcattaatt gtttgctttg gacatgtgga 1200
aagagcctta ctaataaaat tgattttact tatgaaaaaa aaaaaaaaaa 1249

```

<210> 87

<211> 1064

<212> DNA

<213> Homo sapiens

<220>

<221> misc-feature

<223> Incyte ID No.: 1441770CB1

<400> 87

```

cggctctcca gagcgtctgt aaacacccag agactgtcat ggagggggag gaggaggcgg 60
cggcggcgaa gggaggcggt tggggccgcc tccagggtcc gctctgcat tcctgaactg 120
gtccctcgte cccgtgactc tggcatcagg gaagcgaact gttaggcgag aggaggaggc 180
agccagaacc atatccctt cttcctcggg gcggggggccg ggccaggccg gctgagccgg 240
gggagggtc cgggaggggag tgcttgcca ggccggcctg tctgccgca tggatgacag 300
taaggtggtt ggaggcaaaag taaagaagcc cggtaaacgt ggtcggaaag cagccaaaat 360
tgacttgaag gcaaaaacttg agaggagccg gcagagtgc agagaatgcc gagcccga 420
aaagctgaga tatcagtatt tggaaagatt ggtatccagt cgagaaagag ctatatgtgc 480
cctcagagag gaactggaaa tgtacaagca gtggtgcatg gcaatggacc aaggaaaaat 540
cccttctgaa ataaaggccc tactcactgg agaagagcag aacaaatctc agcagaactc 600
aagcaggcat accaaggctg ggaagacaga tgctaatagc aattcctggt gaagattata 660
taaagatgag tcagtgattg aagccaatat tctgattccc atggaagatg gatgggcaag 720
agtgtacttc ttggctccat ttactacct atgctcagta gtcattctctg taaatctgca 780
atttctacca aaatgtgtga tcgtagatct caaaggatct tgctttaact ttcaacactt 840
agaaaaatcta caaacattca gacctgtctg ggttggtatt gccaccatg acatttaaca 900
tgttgtgatg cttgaaaaca caggagtaga gaaaatcgat gaagattgta tttttgcacc 960
ttaactccac attgctttat tggttaattt atattctttc catgtaattc atgtaattgt 1020
atgtctgtgt gtgttttatg tgtcaccacc tttcatgttt ttga 1064

```

<210> 88

<211> 1398

<212> DNA

<213> Homo sapiens

<220>

<221> misc-feature

<223> Incyte ID No.: 1456684CB1

<400> 88

```

agacccaaaa gcattaagga gaaaaagaaa actacatcac ataccagggg agaaataccg 60

```

```

gaggagtcaa actatgttgc tgatcctgga ggatcactga gcaaaaccac aaatattgct 120
gaagaaacca gcaaaattga aacctacatt gcaaaacctg ctctgccggg aacctccaca 180
aatagtaatg ttgcacccct ttgccaaata acagtgaaaa ttggaaacga agccattgtg 240
aaaaggcaca ttctaggatc taaattgttt tataaaagag ggagaagacc caagtatcag 300
atgcaggagg agcctttgcc acaggggaat gaccagaac ccagtggaga cagccactc 360
gggctttgcc aatccgagtg catggagatg agtgaagtgt tcgatgacgc aagtgaccag 420
gattccactg acaaaccgtg gcgcccttac tacaactaca aacccaaaaa gaaatccaga 480
cagttgaaaa aaatgaggaa agtcaactgg aggaaggagc acggaaacag gagcccgagc 540
cataaatgta aatacccagc agaactggat tgcgcctggg ggaaggctcc tcaggataaa 600
ccctttgagg aagaagaaac taaagagatg cccaagctgc agtgtgaact ctgtgatgga 660
gacaaagcag tgggggctgg aaaccaagga agggcccacc gacatcttac ttctcggcca 720
tatgcctgcg agctctgccc caagcagttc cagagccctt ccacactcaa aatgcacatg 780
agatgtcaca ccggggagaa gccataccag tgcaagacct gcggacggtg cttttcgggtg 840
caaggaaact tacagaaaca tgaacgcac cacctgggct tgaaggagtt cgtctgtcag 900
tattgcaaca aggcattcac cttgaatgag accctcaaaa tccatgaaag aatccatact 960
ggagaaaagc gttaccactg tcagttctgc tttcagagat ttttgtatct ctccaccaa 1020
aggaatcacg agcagaggca tattcgggag cataatggga agggctatgc ctgcttccag 1080
tgccccaaaa tttgcaaaac agctgctgcc cttggaatgc accaaaagaa acacttatc 1140
aaaagcccaa gtcagcagga gaaaataggt gacgtgtgcc acgaaaactc aaatcccttg 1200
gagaatcaac atttcattgg ttcagaagac aatgaccaa aggataacat acaaacgggt 1260
gtggaaaatg ttgtcctttg agtggcaaga attagaaaaa tcttcaaaaa tatagtgggt 1320
ggttttttta gttatgattt aagtttagtt tcattttgtc catgtgacag tcatgaagga 1380
gtgaaaaaaa aaaaaaaaaa

```

<210> 89
<211> 746
<212> DNA
<213> Homo sapiens

<220>
<221> misc-feature
<223> Incyte ID No.: 1602916CB1

```

<400> 89
cggctcgagg cgtctttatg ggcccccttt aaggccggcg gaggcattctc gggccgggag 60
cggcgctccg tccgtcgggc gtagecgactg aactgcgcgc ggatccctcc gcggggctcc 120
tcgtccccgt cacgtgactg ttccgtgcag tgccgtgggtg cgaaaatgcc tcgccgggtg 180
gcaccggaga cagccgattt ttacgaccca gcaagaggcc gagctgggtac aatatcctga 240
ctgtaaatcg tccagtggta atattggcga ggaccagac cacttaaate agagctcgtc 300
tccttctcaa atgtttccgt ggatgagacc acaagcagct cctggtagac gaagaggaag 360
acaaacctac agtcgcttcc aaactctaga gttggaaaag gaatttcttt ttaaccctta 420
tctgaccagg aaaagaagaa tcgaggtttc ccacgcctta gccctcaccg agagacaggt 480
aaaaatctgg ttccagaaca ggagaatgaa atggaaaaag gaaaacaaca aggacaaatt 540
tcccgtttcc cggcaggagg tgaaggacgg ggaacgaaa aaggaagccc aagagctgga 600
ggaagacaga gccgaacgct tgacaaatta acttctacct ttaaaattta ccacagacta 660
ttaaaactaa taatcaccat atgctgtgga caccacctat tttctttgtt ggaaaagacc 720
ttactgtgtt tcaagctacc ttcatg

```

<210> 90
<211> 1270
<212> DNA
<213> Homo sapiens

<220>
<221> misc-feature
<223> Incyte ID No.: 1692816CB1

```

<400> 90
gttggtcacg tggttgttcg gagcgggcca gcgaggttag cagggtttta ctgcagagcg 60
cgccgggac tccagcgacc gtggggatca gcgtagggtg gctgtggcct tttgcgaggt 120

```

WO 00/44900

PCT/US00/02237

```

gctgcagcca tagctacgtg cgttcgctac gaggattgag cgtctccacc cagtaagtgg 180
gcaagaggcg gcaggaagtg ggtacgcagg ggcgcaaggc gcacagcctc tagacgactc 240
gctttccctc cggccaacct ctgaagccgc gtcctacttt gacagctgca gggccgcggc 300
ctggctcttc gtgcttcacc atctacataa tgaatcccag tatgaagcag aaacaagaag 360
aaatcaaaga gaataataaa aatagttctg tccaagaag aactctgaag atgattcagc 420
cttctgcatc tggatctctt gttggaagag aaaatgagct gtccgcaggc ttgtccaaaa 480
ggaaacatcg gaatgaccac ttaacatcta caacttccag ccctgggggt attgtccag 540
aatctagtga aaataaaaaat cttggaggag tcaccagga gtcatttgat cttatgatta 600
aagaaaaatc atcctctcag tattggaagg aagtggcaga aaaacggaga aaggcgctgt 660
atgaagcact taaggaaaat gagaaacttc ataaagaaat tgaacaaaag gacaatgaaa 720
ttgcccgcct gaaaaaggag aataaagaac tggcagaagt agcagaacat gtacagtata 780
tggcagagct aatagagaga ctgaatggtg aacctctgga taattttgaa tctactggata 840
atcaggaatt tgattctgaa gaagaaactg ttgaggattc tctagtggaa gactcagaaa 900
ttggcacgtg tgctgaagga actgtatctt cctctacgga tgcaaagcca tgtatatgaa 960
atgcattaat atttgactgt tgagaatttt actgccgaag tttacctcca ctagttcttt 1020
gtagcagagt acataactac ataatgccaa ctctggaatc aaatttcctt gtttgaatcc 1080
tgggacccta ttgcattaaa gtacaaatac tatgtatttt taatctatga tggtttatgt 1140
gaataggatt ttctcagttg tcagccatga cttatgttta ttactaaata aacttcaaac 1200
tcctgttgaa cattgtgtat aacttagaat aatgaaatat aaggagtatg tgtagaaaaa 1260
aaaaaaaaaa                                     1270

```

<210> 91
 <211> 943
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc-feature
 <223> Incyte ID No.: 1968191CB1

```

<400> 91
gtcccatttc cagaaatcac aaggatgtta ggcaatgaat ggagtaaact gcctcctgag 60
gaaaaaacgc gctacctga tgaagcagac agagataagg agcgttacat gaaggaaactg 120
gaacagtatc agaaaacaga ggcctacaag gtcttcagta ggaaaaccca ggaccgtcag 180
aaaggcaaat ctcataggca agatgcagcc cggcaggcca ctcatgatca tgagaaagaa 240
acagaggtaa aggaacggtc tgtttttgac atccctatat ttacagagga attcttgaac 300
catagcaaag ctcggaagc agagctccgc cagcttcgca aatccaacat ggagtttgag 360
gagaggaatg cagccctgca aaagcacgtg gagagcatgc gcacagcagt ggagaagctg 420
gaggtggatg tgatccagga gcggagccgc aacacagctc tacagcagca cctggagacc 480
ctgcggcagg tgctgaccag cagctttgcc agcatgccct tgcttggaa tggagagaca 540
cctacagtgg acaccattga ctcatatatg aacagactgc acagtattat tttagctaat 600
cccaaagaca atgaaaactt catagctaca gttcgagaag ttgtgaacag actcgatcgt 660
tagggaatgg tgagtgtcga ctgataaata tttatatgcc agcacatcat caaaaaataag 720
atgtcatcag actttatcaa tactactaaa accctgggat tacattggat gaacaagttg 780
gagacttggg taagattcct gttgcatggt tgttaaattg agtaaataat attagaaaag 840
agaatcactg tagtcccagc tacttgggag gctgaggtgg gaggattgct tgagcccagc 900
agttcaagtc cagagagatc ctgtctctaa aaataaaaga aaa 943

```

<210> 92
 <211> 1997
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc-feature
 <223> Incyte ID No.: 2052061CB1

```

<400> 92
cgaccacgcg tccgctcgcg tggggcgcgga ggtaccccggt ggggcagcta ggtgcctcca 60
agaaaccccc cccagagga cccgcacgag ttgttgccat ttttcgctga agccctgcc 120

```

WO 00/44900

PCT/US00/02237

```

ctggggggtgg tggtttttctc tatgattcta ccaatcgtcg gaattttttt cctcccttct 180
ttcttttttag gaagggcgctg ggggtgtgcgg cggaaacggc ggcgggtgaag ggatcctctt 240
gtgggtatctc ctccccggag aaatagggga gtggggggccc aagaacgaga agacgagaac 300
gcgtcgccct gcgctatgtc agaattggggc ggggtgtgagg ggaacagctc tcttgcgatc 360
agatcaggag tatgagcctc ccggaggacg gcatgagttc tggacacttc aggagtcctc 420
agctagtgc atggtcgata tggataaaact cataaacaac ttggagggtc aacttaattc 480
agaaggtggc tcaatgcagg tattcaagca ggtcactgct tctgttcgga acagagatcc 540
ccctgagata gaatacacia gtaatatgac ttctccaaca ctctggatg ccaaccccat 600
ggagaaccca gcaactgttta atgacatcaa gattgagccc ccagaagaac ttttggctag 660
tgatttcagc ctgccccaaag tggaaaccagt tgacctctcc ttccacaagc ccaaggctcc 720
tctccagcct ccagggctctg tctgacctc ctctcagagc actggtagcc agcagatctt 780
ccagaccctt gtgggtgtcca cgtcaacatc tgacatgagc acttcagcaa acattcctac 840
tgttctgacc ccagggctctg tctgacctc ctctcagagc actggtagcc agcagatctt 900
acatgtcatt cacactatcc cctcagtcag tctgccaaat aagatgggtg ggctgaagac 960
catcccagtg gtagtgcagt ctctgcccc ggtgtatact actttgctg cagatggggg 1020
gcctgcagtc attacagtcc cactcattgg gggagatggg aaaaatgctg gatcagtga 1080
agttgacccc acctccatgt ctccactgga aattccaagt gacagtgagg agagtacaat 1140
tgagagtggg tctcagcctc tgcagagtct gcagggacta cagcaagaac cagcagcaat 1200
ggcccaaagt caggggagaag agtcgcttga cttgaagaga agacggattc accaatgtga 1260
ctttgcagga tgcagcaaag tgtacaccaa aagctctcac ctgaaagctc accgcagaat 1320
ccatacagga gagaagcctt ataaatgcac ctgggatggc tgctcctgga aatttgctcg 1380
ctcagatgag ctactcgcc atttccgcaa gcacacaggc atcaagcctt ttcggtgcac 1440
agactgcaac cgcagctttt ctctgtctga ccacctgtcc ctgcatcgcc gtcgccatga 1500
caccatgtga gccgcacagg tcacactaga gaagctgctc tgggtatctt cctggtcgtg 1560
tgctgaggtt gggacaattt ttctctctt gacttcagct tgcatatggg gttgaagcag 1620
ccactgagc caagttagg agactggagg aaaagagagc tgggtctccg tggggctctt 1680
catattctac ctccacttct ccactgtcca gacctgtttt tttcaacccc cacatgggtt 1740
gacttccagc gtggcaccca tgggtgcctt cccatcccc cctgttctga aataggggat 1800
ttttccccca gcaacaccac aggaatcaaa ctcaaggctg gcaaccacat ccgctgtttc 1860
ttctctccac tctctcttgc tctctagaac tcttatccaa tgtcttaaca tctaccaaa 1920
agggctcgat gcgttcaca gatttttcac ttcttattgc agggatacat tctgtgtcgc 1980
cacataaggg ttgcttc 1997

```

<210> 93
 <211> 4334
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc-feature
 <223> Incyte ID No.: 2056207CB1

```

<400> 93
cgggtggtggt ggccggggccgg ggcattgagca ggaggaggat taccgctacg aggtgctcac 60
ggccgagcag attctacaac acatggtgga atgtatccgg gaggtcaacg aggtcatcca 120
gaatccagca actatcacia gaatactcct tagccacttc aattgggata aagagaagct 180
aatggaaagg tactttgatg gaaacctgga gaagctcttt gctgagtgtc atgtaattaa 240
tccaagtaaa aagtctcgaa cagccagat gaatacaagg tcatcagcac aggatagtc 300
ttgtcagatc tgctacttga actaccctaa ctctgatttc actggccttg aatgtggaca 360
taagttttgt atgcagtgtc ggagtgaata tttaactacc aaaataatgg aagaaggcat 420
gggtcagact atttctgtgc ctgctcatgg ttgtgatatc ttagtggatg acaacacagt 480
tatgcgcctg atcacagatt caaaagttaa attaaagtat cagcatttaa taacaaatag 540
ctttgtagag tgcaatcgac tgttaaagtg gtgtcctgcc ccagattgcc accatgttgt 600
taaagtccaa tatcctgatg ctaaacctgt tgcgtgcaaa tgtggggccc aattttgctt 660
taactgtgga gaaaattggc atgatcctgt taaatgtaag tgggttaaaga aatggattaa 720
aaagtgtgat gatgacagt aaacctccaa ttggattgca gccaacacaa aggaatgtcc 780
caaatgccat gtcacaattg agaaggatgg tgggtgtaat cacatgggtc gtcgtaacca 840
gaattgtaaa gcagagtttt gctgggtgtg tcttggccca tgggaaccac atggatctgc 900
ctgggtacaac tgtaaccgct ataatgaaga tgatgcaaag gcagcaagag atgcacagga 960
gcgatctagg gcagccctgc agaggtaact gttctactgt aatcgctata tgaaccacat 1020
gcagagcctg cgctttgagc acaactata tgctcaggtg aaacagaaaa tggaggagat 1080
gcagcagcac aacatgtcct ggattgaggt gcagttcctg aagaaggcag ttgatgtcct 1140

```


WO 00/44900

PCT/US00/02237

<223> Incyte ID No.: 2101803CB1

<400> 94

ccgcgccccg	ccgccaccat	gagggccgag	ggcctcggcg	gcctggagcg	cttctgcagc	60
ccggggcaaaag	gccgggggct	gcgggctctg	cagcccttcc	agggtggggga	cttgctgttc	120
tcctgccccg	cctatgccta	cgtgctcacg	gtcaacgagc	ggggcaacca	ctgcgagtac	180
tgcttcacca	ggaaagaagg	attgtccaaa	tgtggaagat	gcaagcaggc	attttactgc	240
aatgtggagt	gtcagaaaga	agattggccc	atgcacaagc	tggaaatgttc	tcccatgggt	300
gtttttgggg	aaaactggaa	tccctcggag	actgtaagac	taacagcaag	gattctggcc	360
aaacagaaaa	tccaccaga	gagaacacct	tcggaaaaat	tgtagctgt	gaaggagttt	420
gaatcacatc	tggataagtt	agacaatgag	aagaaggatt	tgattcagag	tgacatagct	480
gctctccatc	acttttactc	caagcatctc	gaattccctg	acaatgatag	cctcgtagta	540
ctctttgcac	aggttaactg	taatggcttc	acaattgaag	atgaagaact	ttctcatttg	600
ggatcagcga	tatttccctga	tggtgcattg	atgaatcata	gctgttgccc	caatgtcatt	660
gtgacctaca	aaggggacct	ggcagaagtc	agagctgtac	aggaaatcaa	gccgggagag	720
gaggttttta	ccagctatat	tgatctcctg	tacccaacgg	aagatagaaa	tgaccgggta	780
agagattctt	atttctttac	ctgtgagtgc	caggagtgtg	ccaccaagga	caaggataag	840
gccaaagtgg	aaatccggaa	gctcagcgat	cccccaaagg	cagaagccat	ccgagacatg	900
gtcagatatg	cacgcaacgt	cattgaagag	ttccggaggg	ccaagcacta	taaatccccct	960
agtgaagtgc	tggagatctg	cgagctcagc	caggagaaga	tgagctctgt	gtttgaggac	1020
agtaacgtgt	acatgttgca	catgatgtac	caggccatgg	gtgtctgctt	gtacatgcag	1080
gactgggaag	gagccctgca	atatggacag	aaaatcatta	agccctacag	taagcactat	1140
cctttgtact	ccctcaacgt	ggcctccatg	tggttgaagc	tagggagact	ctacatgggc	1200
ctggaacaca	aagccgcagg	ggagaaagcc	ctgaagaagg	ccattgcaat	catggaagta	1260
gctcacggca	aagatcatcc	atatatttct	gagatcaaac	aggaaattga	aagccactga	1320
aactatgcag	catttcagtt	ttcattttaa	cacttagttc	agaaacctta	aaggatttga	1380
atatttcaaa	ttgcacacgt	cactccagca	tctctgtaaa	ataattggaa	tgaaaatact	1440
tcttgacttt	aaacactgca	catgccgtac	tttgagggta	gtctgaatct	tgaaacttta	1500
taccaaatga	atatttgaat	cttttgtttc	ctaagagata	atggcatggt	ttcatatggt	1560
atacttttga	cagacagagt	tttaaaaatg	gaattatttt	ttctttcatg	cctcttgtta	1620
tgttctgaac	aaacttgaat	gatgaaagta	ttaaagagat	atcagtaaaa	agaacaaaaa	1680
ataaagatcc	agaaagaaaa	aaaggg				1706

<210> 95

<211> 1602

<212> DNA

<213> Homo sapiens

<220>

<221> misc-feature

<223> Incyte ID No.: 2112362CB1

<400> 95

ccgtggggca	gtcgaggatg	tcgggtgaatt	acgcggcggg	gctgtcgccg	tacgcggaca	60
agggcaagtg	cggcctcccg	gagatcttcg	accccccgga	ggagctggag	cggaaggtgt	120
gggaactggc	gaggctggtc	tggcagtcct	ccaatgtggt	gttccacacg	ggtgccggca	180
tcagcactgc	ctctggcatc	cccgaacttca	ggggtcccca	cggagtcttg	accatggagg	240
agcgaggtct	ggcccccaag	ttcgacacca	cctttgagag	cgcgcgggcc	acgcagacct	300
acatggcgct	ggtgcagctg	gagcgcgtgg	gcctcctccg	cttccctggc	agccagaacg	360
tggacgggct	ccatgtgcgc	tcaggcttcc	ccaggggacaa	actggcagag	ctccacggga	420
acatgtttgt	ggaagaatgt	gccaaagtgt	agacgcagta	cgtecgagac	acagtcgtgg	480
gcaccatggg	cctgaaggcc	acggggccggc	tctgcaccgt	ggctaaggca	agggggctgc	540
gagcctgcag	gggagagctg	agggacacca	tcctagactg	ggaggactcc	ctgcccagcc	600
gggacctggc	actgcgcgat	gagccagca	ggaacgcoga	cctgtccatc	acgctgggta	660
catcgctgca	gateccggccc	agcgggaacc	tgccgctggc	taccaagcgc	cggggaggcc	720
gcttggtcat	cgtcaacctg	cagcccacca	agcacgaccg	ccatgctgac	ctccgcatcc	780
atggctacgt	tgacgaggtc	atgacccggc	tcattgaagca	cctggggctg	gagatccccg	840
cctgggacgg	cccccggtgt	ctggagaggg	cgctgccacc	cctgccccgc	ccgcccacc	900
ccaagctgga	gcccaggag	gaatctccca	cccggatcaa	cggtctctatc	ccgcggcgcc	960
ccaagcagga	gccctgcgcc	cagcacaacg	gctcagagcc	cgccagcccc	aaacggggagc	1020
ggcccaccag	ccctgcccc	cacagacccc	ccaaaagggt	gaaggccaag	gcggtcccca	1080
gctgaccagg	gtgcttgggg	aggggtggggc	tttttgtaga	aactgtggat	tctttttctc	1140

tctgtggtctc	actttgttac	ttgtttctgt	ccccgggagc	ctcagggctc	tgagagctgt	1200
gtccaggcc	aggggttaca	cctgccctcc	gtggtccctc	cctgggctcc	agggggcctc	1260
ggtgcggttc	cggggaagaag	ccacacccca	gaggtgacag	ctgagccctc	gccacacccc	1320
agcctctgac	ttgctgtgtt	gtccagaggt	gaggtctgggc	cctccctggt	ctccagctta	1380
aacaggagtg	aactccctct	gtccccagggt	cctcccttct	gggcccccta	cagccccacc	1440
taccctcct	ccatggggcc	tgcaggaggg	gagacccacc	ttgaagtggg	ggatcagtag	1500
aggcttgac	tgcttttggc	gctggaggga	gacgtgggtc	caccaggctt	ctggaaaagt	1560
cctcaatgca	ataaaaaaca	tttctttctt	gcaaaaaaaa	aa		1602

```
<210> 96
<211> 1951
<212> DNA
<213> Homo sapiens
```

```
<220>  
<221> misc-feature  
<223> Incyte ID No.: 2117346CB1
```

<400>	96						
gaggcgcgcg	cgaccggcgg	ctcttttggcg	cggattaggg	ggtctcggcg	agggagtc	at	60
caagctttgg	tgtatgtgtt	ggccggttct	gaagtcttga	agaagctctg	ctgaggaaga		120
ccaaagcagc	actcgtttgc	aattagggaa	tggaccgttt	gggttctctt	agcaatgatc		180
ccctctgataa	gccaccttgc	cgaggctgct	cctcctacct	catggagcct	tatatcaagt		240
gtgctgaatg	tgggccacct	cctttttttcc	tctgcttgca	gtgttttact	cgaggctttg		300
agtacaagaa	acatcaaagc	gatcatactt	atgaaataat	gacttcagat	tttctgtcc		360
ttgactcccg	ctggactgct	caagaagaaa	tggccctttt	agaagcttg	atggactgtg		420
gctttggaaa	ttggcaggat	ctagccaate	aaatgtgcac	caagaccaag	gaggagtgtg		480
agaagcacta	tatgaagcat	tgtacaaata	acctctgtt	tgcattctacc	ctgtggaacc		540
tgaacaagc	agaggaagca	aaaactgctg	acacagccat	tccatttcac	tctacagatg		600
acctcccccg	acctaccttt	gactccttgc	tttctcggga	catggccggg	tacatgccag		660
ctcgagcaga	tttcatttag	gaattttgca	attatgcaga	atgggacttg	agagacattg		720
attttggtag	agatgactcg	gacattttac	atgctctgaa	gatggctgtg	gtagatatct		780
atcattccag	gttaaaggag	agacaaagac	gaaaaaaaat	tataagagac	catggattaa		840
tcaaccttag	aaagtttcaa	ttaatggaac	ggcggtatcc	caaggagggtc	caggacctgt		900
atgaaacaat	gaggcgattt	gcaagaattg	tggggccagt	ggaacatgac	aaattcattg		960
aaagccatgc	atttgaattt	gaactccgaa	gggaaatcaa	gaggctccaa	gaatacagga		1020
cagcagcgat	taccaatttt	tgtagtgcga	gaacctacga	tcacctcaag	aagacacggg		1080
aggaagagcg	ccttaaaccgc	actatgtctt	cagaagttct	ccagtataatc	caggacagta		1140
gtgcttgcca	gcagtggctc	cgccggcaag	ctgacattga	ttccggcctg	agtccttcca		1200
ttccaatggc	ttcgaattca	ggtagacgga	gtgcaccacc	cttgaacctc	actggcctcc		1260
ctggcacaga	gaagctgaat	gaaaaagaaa	aggagctctg	ctgagtgtgtg	aggttggtcc		1320
ctggagccta	tttagaatat	aaatctgtct	tattgaacga	atgtaacaag	caaggaggct		1380
taagactggc	gcaggcaaga	gcactcatca	agatagatgt	gaacaaaacc	cggaaaatct		1440
atgatttcc	catcagagaa	ggatacatca	ctaaaggcta	aggctccaag	agcttgggat		1500
cagaagtctag	aagtttggaa	tgtggtgggt	caaaggacaa	tatgggtggg	cattctggag		1560
agtttggtttt	cagctgaatt	ctcatggtga	aaacagggga	aaggacaaag	gaaaccttaa		1620
gttgtattgt	ctactttctt	ctccactctg	ctttaaaaaca	ctcctgttgt	tggattattg		1680
ctgcagagtt	gtgtgctaca	taagctatta	ttaaattgtga	gtgggcattc	attcctaaca		1740
cctcttgtaa	ctaaaagacc	catagtacct	tcacatcaca	gtgcctggga	gaaattggac		1800
ctaaaccacc	agttctgtaa	tcccaggagt	tcaagcctag	aatccttaat	attgtccggg		1860
gaaaggtttt	tctgaataaa	accagggctt	ggccttttaa	aaaactttgg	ggaaacgaat		1920
tttaaaaaatt	aaaaagaaaa	agagtttttt	a				1950

```
<210> 97
<211> 854
<212> DNA
<213> Homo sapiens
```

<220>

WO 00/44900

PCT/US00/02237

<221> misc-feature

<223> Incyte ID No.: 2119917CB1

<400> 97

```

cccacgcgtc cgcggaacggt gggcgcgcgcg tatgacggcc agcgcacagc cgcgcgggcg 60
gcggccagga gtcggagtcg gagtcgtggt gaccagctgc aagcatccgc gttgcgtcct 120
cctggggaag aggaaaggct cggttggagc tggcagtttc caactccctg gaggtcatct 180
ggagttcggg gaaacctggg aagaatgtgc tcaaagggaa acctgggaag aagcagctct 240
tcacctgaaa aatgttcaact ttgcctcagt tgtgaattct ttcattgaga aggagaatta 300
ccattatggt actatattaa tgaaaggaga agtggatgtg actcatgatt cagaaccaa 360
gaatgtagag cctgaaaaaa atgaaagttg ggagtggtt ccttgggaag aactacctcc 420
cctggaccag cttttctggg gactgcgttg tttaaaagaa caaggctatg atccatttaa 480
agaagatctg aaccatctgg tgggatacaa aggaaatcat ctctaggtgg ccgagaagat 540
ttgattttct ttaaaaagac aagaataagg tctggtagg gaatgaaaaa tgtatacatt 600
tcggaacaac tccattttat ctaaaaaagt tcttgtgatt gccagtttat ttgcagctct 660
ttaatgtatc cccactctt tcagccagta cttgagaaaa tttttctgaa atatgtcatt 720
gaattgtatt ccagacacag aatacatgat aaatactgat attatgggta atctgcttct 780
catatttacc tatggatatg tacgtgcaat gtgccataac tagttgagag ggtgggtgag 840
gcagattttc cttt                                     854

```

<210> 98

<211> 1581

<212> DNA

<213> Homo sapiens

<220>

<221> misc-feature

<223> Incyte ID No.: 2123456CB1

<400> 98

```

tccgggaaag tttcttttga ggtccggccc ggagcggcca tgtcccacgg ccccaagcag 60
cccgccgccc cgcccggtcc ggcggggcgg aaggctccgg gccagcatgg gggcttcgtg 120
gtgactgtca agcaagagcg cggcgagggt ccacgcgcgg gcgagaaggg gtcccacgag 180
gaggagcccc gttctgcagc cgggtgaagaa acgcggctgg cccaagggca agaagcggaa 240
gaagattctg ccgaatgggc ccaaggcacc ggteacgggc tacgtgcgct tcctgaacga 300
gcggcgcgag cagatccgca cgcgccaccc ggatctgccc tttcccagaga tcaccaagat 360
gctggggccc gagtggagca agctgcagcc aacggaaaaa cagcgggtacc tggatgagga 420
cgagagagag aagcagcagt acatgaagga gctgcgggcg taccagcagt ctgaagccta 480
taagatgtgc acggagaaga tccaggagaa gaagatcaag aaagaagact cgagctctgg 540
gtcatgaac actctcctga atggacacaa ggggtggggac tgcgatgggt tctccacctt 600
cgatgttccc atcttcaactg aagagttctt ggacaaaaac aaagcgcggtg aggcggagct 660
tcggcgcttg cggaagatga atgtggcctt cgaggagcag aacgcgggtac tgcagaggca 720
cacgcagagc atgagcagcg cgcgcgagcg tctggagcag gagctggcgc tggaggagcg 780
gaggacgctg gcgctgcagc agcagctcca ggcgctgcgc caggcgctca ccgccagctt 840
cgctcactg ccggtgcccg gcacggggcg aacgcccacg ctggggcactc tggacttcta 900
catggccccg cttcacggag ccacgcagcg cgacccccgc cagcacgaga agtcatcgt 960
ccgcatcaag gaaatcctgg ccaggtcgc cagcgagcac ctgtgaggag tggcggggcc 1020
cacgatgcag aggagaagct gtgggcgcgg ccctgccaca cccacccccg tggacgagag 1080
gctgggggtc caccctttgg ggccctggcc catcctgcac cttggggggt ccagcccccc 1140
taaaattaaa tttctgcagc atccctttag ctttcaatct ccccagcccc ctgaaccccg 1200
aaaaagcact cgctgcgcga tacaccacga agaacctcac agccgagggt gcccctcctc 1260
ggaggacagc cacgcgctac actggctctc cgggccaccc ccaggacaca gggcagacga 1320
aaccacccc cagcacacgg caggaccccc caaattactc actacggggg gctgtgccat 1380
aggccacaca ggaagctgcc ttgtggggac ttacctgggg tgtccccgc atgcctgtac 1440
cccagatggg tgggggccgg ctttggccat cctgctctcc tccagccgag ggaccctgg 1500
gggggtggct ccttctcact gctggatccg gactttttta ataaaaacaa gtaaaatttg 1560
tgttttataa aaaaaaaaaa a                                     1581

```

<210> 99

<211> 2150

WO 00/44900

PCT/US00/02237

<212> DNA

<213> Homo sapiens

<220>

<221> misc-feature

<223> Incyte ID No.: 2148792CB1

<400> 99

```

gtctcgatct cctgacctcg ccattccacc gcctcagcca cccgaagtgt tgggatttca 60
ggggccaaat agttgcatca catgtatcta atccgagagt ctcatgcttc tggtagctcc 120
tcagtgaacca gctcctgtct actgccctca gaaagcccaa ccctcaggca atggcggcct 180
tgttctctgt tgcctccacc caggccgagg tgaccttcca ggacgtggct gtgtacctct 240
cccgggagga atggggccgc ctggggccctg ctccagagggg cctctacagg gacgtgatgc 300
tggagacctt cggaaccta gtctcactgg gactaggacc tgcaggcccc aagcctggag 360
tgatctcgca gttggagcga ggggatgagc cctgggtcct ggatgttcag ggcacctctg 420
ggaaagagca cctgagagtc aacagcccag ctcttgggac cagaactgag tacaaggagt 480
tgacttcaca ggagacattt ggtgaggaag atccccaggg atctgagcca gtagaagcct 540
gtgaccacat cagtaagtca gaggggagcc tggaaaagct agtggagcag agaggcccca 600
gggcagtcac actgaccaac ggggagagca gcagggagtc tgggggaaac ctacaggttc 660
tgtcaagacc tgttctctgt cagagacctc acaaattgta tatatgtgag caaagttttg 720
aacagagatc atatctcaac aaccataagc gtgtacacag gtcaaaaaaa acaaatacag 780
ttcgtaactc tggggaaatc ttcatgtcaa acttagttgt taaagaagat cagaaaattc 840
ctactgggaa aaaattgcat tattgcagtt actgtgggaa aacattcagg tacagtgcc 900
accttgtcaa gcatcagcgg cttcacactg aagagaagcc ctacaaatgt gatgagtgt 960
ggaaagcctt cagccagagc tgcgagttca tcaatcaccc aaggatgcac tcaggagaga 1020
ttccctaccg gtgtgacgag tgtgggaaga cattcacccg gaggcccaac ctcatgaagc 1080
accagaggat tcacactggg gagaaaccct acaagtgtgg ggagtgtggg aagcacttta 1140
gcgcctactc ttccctgatt tatcaccaga gaatccacac cggagagaaa ccctataaat 1200
gtaatgactg cgggaaagcc ttcatgtgat gctcaatcct tatccgacat cgtcggactc 1260
acaccggaga gaagccattt gagtgcagg aatgtggcaa aggctttaca caaagtctta 1320
accttatcca acatcagaga attcacactg gagagaaacc ctataaatgt aatgaatgtg 1380
agaaagcttt cattcaaaaa accaaactcg tggaaatca gagaagccac actggagaga 1440
agccctatga atgcaatgac tgtggcaaag ttttcagcca aagcacacac ctcatccagc 1500
accagagaat ccacacagga gagaagccct acaagtgcag cgagtgtggg aaagccttcc 1560
acaacagttc cagactcatc caccaccaga ggctgcacca cggagagaaa ccctacagat 1620
gcagcgattg caagaaagcc ttccagccaga gcacgtactt gattcagcac cggaggatcc 1680
acaccgggga gaagccctac aagtgcagcg agtgtgggaa ggccttcccg cacagtcca 1740
acatgtgtca gcatcagcgg attcacctcc gggaggactt ctccatgtaa cagtggcgcg 1800
gtgtccgagg gcagagtcca gctgagcact tctgcatgc gccccggca cctgactctg 1860
ccctttatgt attatccaca cgatgttttc acagagtgaaggacgtttc tcattaaaca 1920
aacctctttt cttaaataca aaaaaaaaaa agggggggcc gctttagggg tcccaggggt 1980
tcccaacccc taatcctaaa caatgtaata gctgttcccg gtgtaaaatt gttagcggcc 2040
caaaattccc tggcaaatta tcgaaccggg aatccttaaa tgtttaaaac ccccggggtg 2100
gccccaaaaa aggtgtgact cgaaacttcc acattaaaat tcgggggggg 2150

```

<210> 100

<211> 691

<212> DNA

<213> Homo sapiens

<220>

<221> misc-feature

<223> Incyte ID No.: 2751943CB1

<400> 100

```

cggcgccgga gcgggcggtc tggcgcggt cctctggttg ctccggggcc tgacctcgg 60
aactgcgcct cggcgggcgg tgcggggcca agcggggcgg ggcggggccc gcaccgggcc 120
gggactgggg gaggcagggt ctcttgacca agagtgaagt cctcttgcca agagtgaagt 180
gcaaaagaaa ctaaccccg agcagttcta cgtcacaa gaagaggaa cggaaccgcc 240
tttcagtggg atctacctga ataacaagga agcaggaatg tatcattgcg tgtgctgcga 300
cagtcactc ttcatgtctg agaaaaagta ctgctctggc actgggtggc cttcgttttc 360
cgaggctcat ggtacgtctg gctctgatga aagccacaca gggatcctga gacgtctgga 420

```

WO 00/44900

PCT/US00/02237

tacctcgtta	ggatcagctc	gcacagaggt	tgtctgcaag	cagtgtgaag	ctcatctagg	480
tcacgtgttt	cctgatggac	ctgggcccaa	tggtcagagg	ttttgcatca	acagtgtggc	540
tttgaagttc	aaaccaagga	aacactgacc	atcttcaaga	gtccccgttc	cttgccaccc	600
cttcacgtgc	accctcaatt	tccacaattc	acttgaatga	cttggtttat	ttgcaataaa	660
actgggctga	atttgcaaaa	aaaaaaaaaa	a			691

<210> 101

<211> 2101

<212> DNA

<213> Homo sapiens

<220>

<221> misc-feature

<223> Incyte ID No.: 3128913CB1

<400> 101

gtggccttgca	gctcggggtg	ggtggctcat	ttcctggccg	ctcctgggct	tgcgggaaag	60
aagagattac	tcacactcct	tctcaagcac	agaaccagtt	gtactgagct	ttttgctaag	120
ctgttttcagc	caagaatggc	tgtggaatct	ggagtgattt	caaccctgat	acctcaggat	180
cctccggaac	aagaactaat	actagtgaag	gtagaagata	acttttctctg	ggatgagaaa	240
tttaagcaga	atgggagtag	tcaatcctgc	caagaattgt	ttcgtcagca	attcagaaaa	300
ttttgctacc	aggaagacacc	tggggccccg	gaggctctga	gccgactcca	ggaactttgc	360
tatcagtggc	taatgccaga	gttgcacaca	aaggagcaga	tcttagaact	gctgggtactg	420
gagcagttcc	tgagcattct	gcctgaggag	ctgcagatct	gggttcagca	acataatcca	480
gaaagcggcg	aggaagctgt	gaccctgttg	gaggatttag	agagggagtt	tgatgacca	540
gggcagcagg	tcccagctag	tccacaggga	ccagcagtag	catggaagga	tttaacatgt	600
ctcagagcat	cccaagagtc	aacagacatc	cacctccagc	ccttaaagac	acagctgaaa	660
tcctggaaac	catgcctttc	ccctaaaagt	gattgtgaga	acagtgaaac	agcaacaaaa	720
gagggcatct	cagaagaaaa	atcacaggga	ctccctcagg	aaccttcatt	tcgagggaatt	780
agtgtgcatg	aaagcaattt	agtgtggaag	caagggaagt	ctacagggga	gaaactaaga	840
tctccttccc	aagggggcag	ttttagtcaa	gtgatcttca	caaacaaatc	tctaggaaag	900
agagaccttt	atgatgaggc	tgaaagatgc	ttgattctaa	ctacagactc	tataatgtgt	960
cagaaagttc	ctccagaaga	gagaccttat	agatgtgatg	tatgtgggca	cagcttcaag	1020
cagcattcct	ctctaacaca	acatcagaga	atccatactg	gagaaaagcc	ctataaatgt	1080
aaccagtgtg	ggaaggcctt	tagtttgagg	tcctatctta	ttattcatca	gagaattcat	1140
agtgggtgaga	aagcatatga	atgtagtga	tgtgggaaag	ctttcaatca	gagctcagcc	1200
ctcattagac	atcgggaaat	ccatactggg	gagaaaagct	gtaaatgtaa	tgagtgtggc	1260
aaagcattga	gtcaaagttc	atatctcatt	atacatcaaa	gaattcacac	tggtgagaaa	1320
ccttatgtag	gtaatatg	tgggaaaacc	tttagccaga	gctcaaaact	cattagacat	1380
cagcgaattc	acacaggaga	gagaccctat	gaatgtaatg	aatgtggaaa	agctttcagg	1440
cagagctcag	agctgattac	tcacagaga	atacatagtg	gagagaaacc	ctatgaatgt	1500
agtgaatgtg	gaaaagcttt	cagtttgagc	tcaaaccctta	tcagacatca	gagaattcat	1560
agtggggagg	aaccttatca	gtgtaatgaa	tgtggcaaaa	ctttcaaaaag	gagctcagcc	1620
cttggttcagc	atcagagaat	tcattctggg	gatgaagctt	atatatgtaa	tgaatgtggg	1680
aaggctttca	ggcacagatc	ggtccttatg	cgccatcaaa	gagtcacac	tataaagtaa	1740
tttgtgaata	ctgtgaatag	tgtaaatact	tcagtcagat	ttttaagttt	gttagtcaaa	1800
agagtttact	ttggagcaaa	actccataaa	ggttataaaa	tactaggtct	tgagtctagc	1860
ttgctttgtg	cagcatttcc	cagtgtcta	gtaaagtgtc	ccttgaaagc	ttttcctgtg	1920
actaatcaga	acagaatata	gaagaatcat	tacttccagc	tcttctctta	ttaggaatac	1980
tcaggaaata	cgaaaagtgg	gaatgtata	ttgaaacctc	attttgtatg	aaagtgtcat	2040
gaatatagca	acccaggctc	tgtcactgca	tctgattgtt	agtgtgccag	gttatggggg	2100
g						2101

<210> 102

<211> 2196

<212> DNA

<213> Homo sapiens

<220>

<221> misc-feature

<223> Incyte ID No.: 3282941CB1

ccgccatgat tgtaagtttc tcgagtcctc cccagccatg cgtcctgtac aacctgtgga 720
accaggcagc caaanncagt natagttgt 749

<210> 104
<211> 1311
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 1294
<223> a or g or c or t, unknown, or other
<223> Incyte ID No.: 3490802CB1

<400> 104
gggcctttgt ttctcgtgc agcgggagct ccaggtttat cctctgtgtt ctgtgtcctg 60
tgcttataga ggcccgctct ctgtggccgt gtgacctgca agtattggga gagccacagc 120
taaaccgccg gaccctgga agcctagaaa tgggaccatt gcaatttaga gatgtggcca 180
tagaattctc tctggaggag tggcattgcc tggacactgc acagcggaat ttatataggg 240
atgtgatgtt agagaactac agaaacttgg tcttccttgg tattgttgtc tctaagccag 300
acctggttac ctgtctggag caaggaaaaa aacctttaac tatggaaaga catgagatga 360
ttgccaaacc cccagttatg agttctcatt ttgcccaaga cctttggcca gagaacatac 420
aaaattcttt ccaaataagg atgttgagaa gatatgaaga atgcagacat gacaatttac 480
agttaaaaaa aggcgtgtaa agcgtgggtg agcataaggt gcacaaagga gggtataatg 540
gacttaacca atgtttgaca actaccacaga aagaaatatt tcaatgtgat aaatatggaa 600
aagtctttca taagttttca aattcaaaca catataagac aagacatact ggaataaatc 660
ttttcaaatg tataatatgt ggcaaaagctt ttaaaccgtc ctcaaccctt actacacata 720
agaaaaattc tactggagag aaaccttaca aatgtgaaga atgtggcaaa gcttttaacc 780
aatcctcaaa ccttactaca cataagagaa ttcatactgg agagaaacct tacaatgtg 840
aagaatgtgg caaagctttt aactggtcct cagaccttaa taaacataag aaaattcata 900
ttgaacgaaa accctacata gtgaagaatg tgacagatct tttaaatgtt cctccacttt 960
taattagcat aagataattc atactggaga gaaaccctat gaatgtgatg aatgtgggaa 1020
agcctttaac cagcctcgca ctcttagtaa atttgagagt ttatatggaa cacaaccct 1080
acaaatataa agaatgtgac aaagcttttt aaggaagttc tcaaccctta ttacacataa 1140
ttcataccaa acagaagccc tacaagtgtg aagaatgtgg caaaacctat aaacctataa 1200
caagttctca attccttttt ttttgagatg gagtttcact cttgtcaccg aggcagaggt 1260
tgcagtgagc actccagtc aggcgacaga gtangccttg tcgcgatccc a 1311

<210> 105
<211> 990
<212> DNA
<213> Homo sapiens

<220>
<221>
<223> Incyte ID No.: 3507366CB1

<400> 105
caaaaaggaa agaataaggc aaattcttag aatgtatgca caacttaata tccttgctcg 60
tttgatgtgc attgatctca tttaataggt ttttgaatct gaaaattcaa gaagggtgaag 120
ctcacacat tttttgccct gcatatgatt gcttccaact tgtacctgtg gatatcatag 180
aaagtgtagt ttcaaaggag atggacaaac gatacctaca gtttgatatt aaggcctttg 240
ttgaaaaata tcctgccatt aaatgggtgc ctactccagg ctgtgacaga gcagtaagac 300
taacgaaaca aggggtcaaat acatctggat ctgatacact cagcttccca ttgctgagag 360
ctcctgctgt tgattgtgga aaaggacacc tctctgctg ggagtgcctt ggtgaagcac 420
atgagccttg tgactgccaa acatggaaga attggctgca aaaaataaacc gaaatgaaac 480
cagaagaact tgtgggagtt agtgaagcct acgaggatgc cgccaattgt ctctggttat 540
taactaactc caagccttgt gccaactgta agtctccaat acagaagaat gaaggctgca 600
atcacatgca gtgtgctaag tgcaagtatg acttttgctg gatttgctt gaagagtggga 660
aaaaacatag ttcgtccact ggaggttatt acagatgtac tcgctatgaa gtcattcaac 720
acgtggagga gcaatccaag gaaatgactg tggaggctga gaaaaaacac aaacgatttc 780


```

aggaacttga cagatttatg cactattata caagatttaa aaaccatgag catagttatc 840
agctagaaca acgccttctt aaaacagcca aagaaaagat ggagcaaagt agcagagtct 900
caaagaactg aaggaggctg tccagatacc actttcattg gagatgagtt catgtgctct 960
aaaaatcggc gcattctcaag tgtcttatca                990

```

<210> 106
 <211> 1048
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc-feature
 <223> Incyte ID No.: 3573060CB1

```

<400> 106
ccgctgcagc tctccgcggg acatctcacc gttctggaga cagggctcgc tcgctctcac 60
ggcttcttag gccgggggtg gacagccgcc ttccggccag aggggatgag gttgcgctgc 120
gctccgggag cgccgatggc gtgactggcc ccgcgcggag cagcgacact gcccggccag 180
cccgtttctc tgcccgagc catgaatctc agtagcgcca gtagcacgga ggaaaaggca 240
gtgacgaccg tgcctctggg ctgcgagctc agtcaggaga ggccgacttg gaccttcaga 300
ccccagctgg aggggaagca gagctgcagg ctgttgcttc atacgatttg cttggggggag 360
aaagccaaag aggagatgca tcgcgtggag atcctgcccc cagcaaacca ggaggacaag 420
aagatgcagc cggtcaccat tgctcactc caggcctcag tctccccat ggtctccatg 480
gtaggagtgc agctttctcc cccagttact ttccagctcc gggctggctc aggaccctg 540
ttcctcagtg gccaggaacg ttatgaagca tcagacctaa cctgggagga ggaggaggaa 600
gaagaagggg aggaggagga agaggaagag gaagatgatg aggatgagga tgcagatata 660
tctctggagg agcaaagccc tgtcaaacaa gtcaaaaggc tggtgcccca gaagcaggcg 720
agcgtggcta agaaaaaaa gctggaaaaa gaagaagagg aaataagagc cagcgttaga 780
gacaagagcc ctgtgaaaaa ggccaaagcc acagccagag ccaagaagcc aggattcaag 840
aaatgaggag ccacgccttg gggggcacgg tgcaaagtgg gccttccttg ggctgtgctg 900
caggcacagg gtgcccctgt ccagcccctc cactgtgttc tgaatgcaac aggggtgttg 960
cgggggcaac atgagagccc ctcaccccc actctccact ttcaggaggc cccagtgaa 1020
gagccccacc tcgggtcaca ataagtgt                1048

```

<210> 107
 <211> 1349
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc-feature
 <223> Incyte ID No.: 3573661CB1

```

<400> 107
gagaaagcag agctatttca agagtgaagg acagaaggga atccagaggc catctaagcg 60
aggaagggtc tacaggcagt gaggtaaggc caggagcagg gccaggcca ggcacgacca 120
ccgaggggat gaacttcaca gtgggtttca agccgctgct aggggatgca cacagcatgg 180
acaacctgga gaagcagctc atctgcccc tctgcctgga gatgttctcc aaaccagtgg 240
tgatcctgcc ctgccaacac aacctgtgcc gcaaatgtgc caacgacgtc ttccaggcct 300
cgaatcctct atggcagtc cggggctcca ccactgtgtc ttcaggaggc cgtttccgct 360
gcccacgtg caggcatgag gttgtcctgg acagacacgg tgtctacggc ctgcagcgaa 420
acgtgctagt ggagaacatt atcgacattt acaagcagga gtcattcaag ccgctgcact 480
cgaaggctga gcagcacctc atgtgcgagg agcatgaaga agagaagatc aatatttact 540
gcctgagctg tgagggtgcc acctgctctc tctgcaaggc cttcgggtgcc cacaaggact 600
gtgagggtgc cccactgccc accatttaca aagccagaa gaggtagctc agcgatggca 660
tcgcgatgct ggtggcaggc aatgaccgag tgcaagcagt gatcacacag atggaggagg 720
tgtgccagac tatcgaggac aatagccgga ggcagaagca gttgttaaag cagaggtttg 780
agagcctgtg cgcagtgtcg gaggagcgca agggtagct gctgcaggcg ctggcccggg 840
agcaagagga gaagctgcag cgcgtccgag gcctcatccg tcagtatggc gaccacctgg 900
aggcctcctc taagctggtg gagtctgcc a tccagtccat ggaagagcca caaatggcgc 960

```

WO 00/44900

PCT/US00/02237

tgtatctcca gcaggccaag gagctgatca ataagggtcgg ggccatgtcg aagggtggagc 1020
 tggcagggcg gccggagcca ggctatgaga gcatgggagca attcaccgta aggggtggagc 1080
 acgtggccga aatgctgcgg accatcgact tccagccagg cgcttccggg ggaggaagag 1140
 gaggtggccc cagacggaag aagagggcaa cccggggggc ggaagaaaaa acggcccgga 1200
 tggggcetta taggcctttg cggccgaacc cggacccccct gcttcgaaaa agcccccggc 1260
 gcttaagaat ttccggggga aggaattctt gccgcaaaaa aacccccggca agcttttaac 1320
 ccccaaaaat tccgggggcgc ccggggccc 1349

<210> 108
 <211> 1642
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc-feature
 <223> Incyte ID No.: 3633422CB1

<400> 108
 ctagtcttag atcgcgagcg cccgcccagg caccaccagg cggcgccgac ctcagcgcg 60
 acctatgggc tcgctaccag gacatgcgga gactgggtgca cgacctctcg ccccccgagg 120
 tctgcagtct cctgaaccca gcagccatct acgccaacaa cgagatcagc ctgctgacg 180
 ttgaggtcta cggctttgac tacgactaca ccctggccca gtatgcagac gcaactgcacc 240
 ccgagatctt cagtaccgcc cgtgacatcc tgatcgagca ctacaagtac ccagaaggga 300
 ttccggaagta tgactacaac cccagctttg ccctccgtgg cctccactat gacattcaga 360
 agagccttct gatgaagatt gacgccttcc actacgtgca gctggggaca gcctacaggg 420
 gcctccagcc tgtgccagac gaggaggtga ttgagctgta tgggggtacc cagcacatcc 480
 cactatacca gatgagtggc ttctatggca aggggtccctc cattaagcag ttcatggaca 540
 tcttctcgct accggagatg gctctgctgt cctgtgtggt ggactacttt ctgggccaca 600
 gcctggagtt tgaccaagca catctctaca aggacgtgac ggacgccatc cgagacgtgc 660
 atgtgaaggc cctcatgtac cagtggatcg agcaggacat ggagaagtac atcctgagag 720
 gggatgagac gtttctgtgc ctgagccgcc tgggtggccca tgggaaacag ctgttctctca 780
 tcaccaacag tcttttcagc ttctgtagaca aggggatgag gcacatgggtg ggtcccgatt 840
 ggcgccagct ctctgatgtg gtcattgtcc aggcagacaa gcccagcttc ttcactgacc 900
 ggcgcaagcc tttcagaaaa ctogatgaga agggctcact tcagtgggac cggatcacc 960
 gcttgaaaaa gggcaagatc tatcgccagg gaaacctgtt tgacttctta cgcttgacgg 1020
 aatggcggtg ccccgcggtg ctctacttcc gggaccacct ctatagtgtat ctggcggtatc 1080
 tcatgctgag gcacggctgg cgcacaggcg ccctcatccc cgagctggag cgtgagatcc 1140
 gcatcatcaa cacggagcag tacatgcact cgtgacgtg gcagcaggcg ctcacggggc 1200
 tgctggagcg catgcagacc tatcaggacg cggagtgcag gcagggtgct gctgcctgga 1260
 tgaaagagcg gcaggagctg aggtgcatca ccaaggccct gttcaatgag cagttcggga 1320
 gcatcttccg cacttccac aacccacct acttctcaag gcgcctctg cgttctctg 1380
 acctctacat ggcctccctc agctgcctgc tcaactaccg cgtggacttc acctctacc 1440
 cagccgtac gccgctgcag cagcaggcac ccctctggat ggaccagctc tgcacgggt 1500
 gcatgaagac ccccttctt ggtgacatgg cccacatccg ctgagggcac ctttattgtc 1560
 tgggacagcg cctcagcccc tctgccccca tccacccaga caagcaataa aagtgggtctc 1620
 ctccctgaaa aaaaaaaaaa aa 1642

<210> 109
 <211> 1818
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc-feature
 <223> Incyte ID No.: 3993377CB1

<400> 109
 gaagactctc tggagccctt caactctctg gcaccagagc cagtgagtgagg aggactatat 60
 ggtattgatg acacggagct gatgggtgca gaggacaagc tgccctctga ggacagccct 120
 gtgattgctg cccttgattg cccttccctc aataatgcta ctgccttcag tctcctggca 180
 gatgatagtc aaacatcaac ctctatcttt gccagtccca cctctccacc tgtcctaggg 240

WO 00/44900

PCT/US00/02237

gagtctgtcc	tgcaagataa	cagctttgac	ctgaataatg	gtagtgacgc	tgaacaggaa	300
gaaatggaaa	ctcaatcttc	agacttccca	ccatccctga	cccagccagc	tcctgatcag	360
tcateccacta	ttcagctaca	tccagcaacc	tcaccagcag	tctcgccaac	aacctcccca	420
gcagttctccc	tagtggtttc	tccagcagcc	tccccagaaa	tctctccaga	agtttggtccc	480
gcagctttcta	cagttgtctc	tccagcagtc	ttctcagtg	tctctccagc	ttcctcagca	540
gtcctcccccag	cagttctctt	agaagtcccg	ttgacggctt	cagtgacatc	cccaaaagcc	600
tctccccgtaa	cttccccagc	agctgccttt	ccaacagcct	ccccagcaaa	taaggatgtc	660
agcagctttc	tagaaaaccac	tgctgacgtg	gaagagatca	ctggagaagg	actcactgct	720
tctggttagtg	gtgatgtcat	gaggagacgt	attgctaccc	cagaagaagt	tcgtcttccc	780
ctccaacatg	ggtggcggag	agaggtgcgc	atcaagaaca	gcagccaccg	atggcagggg	840
gagacctggt	attatggccc	ctgtgggaag	aggatgaagc	aatttccaga	agtgatcaag	900
tacctgagcc	gcaacgtggt	acacagtgtc	cgccgagagc	acttcagctt	cagttccccgt	960
atgectgttg	gagatttctt	tgaagaaaaga	gacacgccag	agggcttgca	gtgggtgcag	1020
ctctcagcag	aggagatccc	gtcgaggatt	caggcaatta	ctggcaaacg	gggtcgacct	1080
cgaaacactg	agaaggctaa	gactaaggaa	gtcccccaagg	tgaaacgggg	tcgaggtcgg	1140
ccacctaaagg	tcaaaatcac	tgagctattg	aacaagacag	acaaccgccc	cctaaagaaa	1200
ctggaggccc	aagaaacatt	gaatgaggag	gataaagcaa	agattgctaa	aagcaagaag	1260
aagatgaggc	agaaggttca	acggggagag	tgctcagacta	ctatccaagg	gcaggccaga	1320
aataagcggga	aacaagagac	caagagctta	aagcagaagg	aagctaagaa	gaaatccaag	1380
gctgagaaaag	aaaaaggaaa	gacaaaagcag	gaaaaactga	aggaaaaagt	caagaggggaa	1440
aagaaggaga	aggtaaaaaat	gaaggaaaag	gaggagggtga	ccaaagccaa	gccagcctgt	1500
aaagcagata	agaccctggc	cacacagagg	cgcttgagg	aacggcagag	gcagcagatg	1560
atcttggagg	acatgaagaa	gccgacagag	gatattgtgtc	tgactgacca	ccagccccgt	1620
cctgacttct	cacgagtccc	tggtctgaca	ttgcccagtg	gagccttctc	agactgcttg	1680
accattgtgg	agttcctgca	tagctttggc	aaggtgctgg	gccttgatcc	tgcccaagggt	1740
tgtgcctagc	ctgggggggtc	ctgcaggaag	gggctcctgt	gttcaagggtg	accactctgg	1800
gtgaagggtgc	aaaacccg					1818

<210> 110
 <211> 785
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> unsure
 <222> 738
 <223> a or g or c or t, unknown, or other
 <223> Incyte ID No.: 4717936CB1

<400> 110						
gtctctgtag	tcattgaggct	gaaggggggtg	gggacagtgt	tgataaaagg	cactagaggc	60
agctcccaca	cccttctctg	gaactgttgc	ccacatgcag	ccccggacac	agccccctagc	120
ccaaacccta	cccttcttcc	tcggagggggc	ccctcgagac	actgggctgc	gggtgcctgt	180
cattaagatg	ggcacagggt	gggaggggctt	ccagcggacc	ctgaagggaag	tcgcctacat	240
cctcctctgc	tgctgggtgta	tcaaggaact	gctggattaa	tggtagcagg	gaactgcctc	300
ctctccccac	cagcaccatg	gctggcatcg	ctcagggtggg	cagggtagag	taaacaggag	360
gcatagctgc	agcttctgtg	gcagagcttg	ccttagcttc	tcattctctt	cttttagcccc	420
cagcccaatt	gccatcaaga	ctcctgaagc	cagctgtgct	tgaccaagga	tgggccataa	480
acaatgagta	aacagtaaaag	tgtggatcct	gctttgagct	gtgtcatcta	gcagacctgc	540
ctcatctctg	agcctccttc	attcccaacc	cctgcctctg	gtggacctct	gggtggcagg	600
agcttggact	gctctggcta	ggaccccgag	aagattgtgg	caagacctgg	cactcctcca	660
agcttggcac	agtgagccca	ccagctcaga	tggttgatct	taccataccc	tcatagtacc	720
aagaatggac	tgcccccnta	agaaacctgt	ttgagaatca	ctgaattata	aatataaacc	780
cagat						785